

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2003, 22:58:15 : Search time 142 Seconds

(without alignments)  
6216.664 Million cell updates/sec

Title: US-09-977-260-1

Perfect score: 2000  
Sequence: 1 ctcgtcccaagtgtgcagc.....atcttaaggaactcttaaaaa 2000

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued\_Patents\_NA.\*  
2: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2000	100.0	2000	US-08-426-509A-1	Sequence 1, Appli
2	2000	100.0	2000	US-08-232-545-1	Sequence 1, Appli
3	2000	100.0	2000	PCT-US95-05008-1	Sequence 1, Appli
4	1909.8	95.5	1987	US-08-876-882-1	Sequence 1, Appli
5	1909.8	95.5	1987	US-09-315-928-1	Sequence 1, Appli
6	1903.4	95.2	1942	US-08-604-989A-11	Sequence 11, Appli
7	1519.4	76.0	1521	US-08-604-989A-10	Sequence 10, Appli
8	1398	69.9	1398	US-08-604-989A-9	Sequence 9, Appli
9	1377	68.8	1713	US-09-741-154-1	Sequence 1, Appli
10	738	36.9	738	US-08-604-989A-8	Sequence 8, Appli
11	455	22.8	16389	US-09-741-154-3	Sequence 3, Appli
12	225	11.2	225	US-08-604-989A-7	Sequence 7, Appli
13	212.4	10.6	1611	US-07-820-011A-3	Sequence 3, Appli
14	212.4	10.6	1611	PCT-US93-00445-3	Sequence 3, Appli
15	199.2	10.0	1602	US-07-820-011A-1	Sequence 1, Appli
16	199.2	10.0	1602	PCT-US93-00445-1	Sequence 1, Appli
17	192	9.6	192	US-08-604-989A-6	Sequence 6, Appli
18	185	9.2	1574	US-09-173-581-12	Sequence 12, Appli
19	185	9.2	1574	US-09-420-915-12	Sequence 12, Appli
20	181.8	9.1	3623	US-08-306-691B-35	Sequence 35, Appli
21	170.4	8.5	1467	US-09-579-182-2	Sequence 2, Appli
22	168.8	8.4	1467	US-09-099-053-1	Sequence 1, Appli
23	165.8	8.3	2674	US-08-817-180-1	Sequence 1, Appli
24	162	8.1	5993	US-09-383-630-1	Sequence 1, Appli
25	162	8.1	5993	US-09-383-630-2	Sequence 2, Appli
26	151.2	7.6	2647	US-09-220-132-77	Sequence 77, Appli
27	151.2	7.6	2647	PCT-US93-06251-77	Sequence 77, Appli

28	148.8	7.4	2049	US-09-099-749-10	Sequence 10, Appli
29	148.8	7.4	2433	US-09-620-312D-830	Sequence 830, App
30	148.8	7.4	2598	US-09-417-197-110	Sequence 110, App
31	148.8	7.4	2616	US-09-417-197-108	Sequence 108, App
32	148	7.4	2469	US-08-459-236-1	Sequence 1, Appli
33	146.4	7.3	933	US-08-701-191A-4	Sequence 4, Appli
34	146.4	7.3	1056	US-08-701-191A-5	Sequence 5, Appli
35	146.4	7.3	2469	US-07-997-133-2	Sequence 2, Appli
36	146.4	7.3	2469	US-07-997-133-2	Sequence 2, Appli
37	146.4	7.3	2662	US-08-451-832A-14	Sequence 14, Appli
38	146.4	7.3	2662	US-08-323-430-14	Sequence 14, Appli
39	146.4	7.3	2733	US-08-371-001-14	Sequence 14, Appli
40	146.4	7.3	2733	PCT-US96-00331-14	Sequence 14, Appli
41	137.6	6.9	1491	US-09-006-675-1	Sequence 1, Appli
42	137.6	6.9	1491	US-09-228-603A-1	Sequence 1, Appli
43	136.6	6.8	3945	US-09-016-434-1404	Sequence 1404, Ap
44	136.6	6.8	3969	US-08-436-044-5	Sequence 5, Appli
45	136.6	6.8	3969	US-08-222-616-23	Sequence 23, Appli

#### ALIGNMENTS

RESULT 1  
US-08-426-509A-1  
Sequence 1, Application US/08426509A

Patent No. 6326469

GENERAL INFORMATION:

APPLICANT: Ullrich, Axel

APPLICANT: Gishizky, Mikhail

APPLICANT: Sures, Irman G.

TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN

TITLE OF INVENTION: TYROSINE KINASES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York,

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,509A

FILING DATE: 21-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/232,545

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-0074-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2000 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

US-08-426-509A-1

Query Match

Best Local Similarity

Matches 2000; Conservative

Score 2000; DB 4; Length 2000;

Pred. No. 0;

Mismatches 0; Indels 0; Gaps 0;

~ April 1994

QY 1 CTCGCTCAAGTTGTCTACAGCCGGACCGCTCGGGGTGTGACAGCCGGCTCGGGAGAGCC 60  
 DB 1 CTCGCTCAAGTTGTGTACAGCCGGACCGCTCGGGGTGTGACAGCCGGCTCGGGAGAGCC 60  
 QY 61 TCTTGAGGGAGGG 120  
 DB 61 TCTTGAGGGAGGG 120  
 QY 121 AGGCTGGGTTCAGTGGACACCAAGCTTCCCTACCTGTGTGACAGCCGGCTGTGTGGA 180  
 DB 121 AGGCTGGGTTCAGTGGACACCAAGCTTCCCTACCTGTGTGACAGCCGGCTGTGTGGA 180  
 QY 181 GGGCATTCAGAGGTGCTGAGAGTGTGACAGTGTGTGACAGTGTGTGACAGTGTGTGAC 240  
 DB 181 GGGCATTCAGAGGTGCTGAGAGTGTGACAGTGTGTGACAGTGTGTGACAGTGTGTGAC 240  
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 DB 241 TTTCCCTGTGGGGGGGATGGCGGGGAGAGGCTCTGTGGTTCTGTGGGGGATTTTCAG 300  
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 DB 301 GGTGTGATTTCTGTGAGAACTTCCCGGGGTGAGCCCGCTTCTCCGAGCCTGGACCC 360  
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 DB 361 CCCCTCCGCTTACAGCAGATGCTCAACAGAGGGGGGGGGGGGGGGGGGGGGGGGGGG 420  
 QY 421 CCAAAATGCGAGACACCCCGCCCAAGCGAGGGAGTGGGCTTCGCGAAGGGGGAGGTGG 480  
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 QY 481 TCACATTCCTGAGAGGCTTCGAGAAACAGAGTGTACCGGCTCAAGACACACAGTGTG 540  
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 DB 601 CCAAGCTCAAGCTCATAGCGGTGTGACAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 660  
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 DB 661 ACCTGAGGCTTCCGAGAGTGTGGGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 720  
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 DB 841 ATTACAGCAAGAGCAAGGGGCTATCTGTGACCAAGCTGTGTGAGAGTGTGAGAGTGTGAGAG 900  
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 DB 961 TGACATTTGGAGACACAGATCGAGAGAGAGTGTGGAGTGTGTGAGAGTGTGTGAGAGTGTGTG 1020  
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 DB 1021 TGGGGCAAAAGGTGGGGGTGAAGAAATATCAAGTGTGTGAGAGTGTGTGAGAGTGTGTGAGAG 1080  
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DB 1081 ACGAGAGGGCGGTATGACGAAGATGCAACACGAGAACTGTGGCTTCTGTGGGGCTGA 1140  
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 DB 1141 TCTGACACAGGGGGCTGTATGATGTGATGAGACAGTGTGAGAGTGTGTGAGAGTGTGTGAGAGT 1200  
 QY 1201 TTTCTGGGAGCCGGGGGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 1260  
 DB 1201 TTTCTGGGAGCCGGGGGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 1260  
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 DB 1261 AGTGTGCGAGGGGATGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1320  
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 DB 1321 CCCGCAACATCTGTGCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 1380  
 QY 1381 AAGCCGAGGGAAGGGGCTAGACTCAAGCCGGCTGCGCTCAAGTGTGAGAGTGTGAGAGTGTGAGAG 1440  
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 DB 1441 CTCTCAAAACAGGGGAAGTGTACCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1500  
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 DB 1621 TCTCATGAGACACTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1680  
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 DB 1681 CCGAGAGGCTGCGGGGAGCTACGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1740  
 QY 1741 ACGCCGAGGCTTCCAGCTTCCCGGAGAGCCGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1800  
 DB 1741 ACGCCGAGGCTTCCAGCTTCCCGGAGAGCCGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1800  
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 DB 1801 TGGCCCCAGAGACGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1860  
 QY 1861 AGGCTCAGGCGGGGCAAGTATCTCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1920  
 DB 1861 AGGCTCAGGCGGGGCAAGTATCTCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1920  
 QY 1921 GGGCTGGGGCGGGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1980  
 DB 1921 GGGCTGGGGCGGGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1980  
 QY 1981 ATTCTAAGGACTTAAAAA 2000  
 DB 1981 ATTCTAAGGACTTAAAAA 2000

RESULT 2  
 US-08-232-545-1  
 ; Sequence 1, Application US/08232545  
 ; Patent No. 6506578  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ulrich, Axel  
 ; APPLICANT: Gishitsky, Mikhail  
 ; APPLICANT: Sures, Iman G.  
 ; TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine

TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,545  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)90-9090  
TELEFAX: (212)869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2000 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA  
US-08-232-545-1

Query Match 100.0%; Score 2000; DB 4; Length 2000;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTCCTCTCCAAAGTTGTGACGCGGGAGACCGCTCGGGGTTGTGACGCGCGGTCCGCGAGCGCC 60  
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DB 61 TCCTGCGGGGGCGGGCGGGGCGGCTCGGGGGCGGCCCTTGAGCAGAAAAAGAAAGAAC 120  
QY 121 AGGCTGGTCCAGTGGGACCCAGCTCCCTACCTCTGTGCGAGCGCGCTGGCTGTGCA 180  
DB 121 AGGCTGGTCCAGTGGGACCCAGCTCCCTACCTCTGTGCGAGCGCGCTGGCTGTGCA 180  
QY 181 GGGCATTCGCGAGCTGCCCGGAGTGTGACCACTTGTCTAGTGTGCTCTACCTGCTCTAG 240  
DB 181 GGGCATTCGCGAGCTGCCCGGAGTGTGACCACTTGTCTAGTGTGCTCTACCTGCTCTAG 240  
QY 241 TTTTCTCTGTGGGGGCGATGGCGGGGCGAGGCTCTGTGTTTCTGTGGGGGCGATTTCAG 300  
DB 241 TTTTCTCTGTGGGGGCGATGGCGGGGCGAGGCTCTGTGTTTCTGTGGGGGCGATTTCAG 300  
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DB 301 GCTGTGATTCTGTGAGGAATTCGCCGGGTGAGCCCCCGGTTCTCTCGAGCTTGGCAC 360  
QY 361 CCGCTCCGCTGAGCGAGATGCGAAGAGCGCTGGGCGCGGGGCGACCCAGTGTATCA 420  
DB 361 CCGCTCCGCTGAGCGAGATGCGAAGAGCGCTGGGCGCGGGGCGACCCAGTGTATCA 420  
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DB 481 TCACCAATCTGAGAGGCTGCGAGAAACAAGAGCTGTGTAACCGGTCAAGACCAACAACGTG 540  
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DB 721 ACTACGTCTGTGCTGAGCTTTTGGCCCGACGTCATCATCTACCGGCTGCTGCACCGCG 780  
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DB 781 ACGGCACTCACAATCGATGAGCGCGTTCCTTCGCAACCTCATGGAATGTGGAGC 840  
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DB 841 ATTACAGCAAGACAAAGGGCGCTATCTGCACCAAGCTGGTGAGACCAAAAGCGAAACAG 900  
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DB 901 GGACCAATTCGGCCGAGAGAGAGCTGGCCAGGGCGGGCTGTACTGAACCTGCACGATT 960  
QY 961 TGACATTGGAGACAGATCGGAGAGAGAGATTGGAGCTGTCTGCAAGGTTGAGTACC 1020  
DB 961 TGACATTGGAGACAGATCGGAGAGAGAGATTGGAGCTGTCTGCAAGGTTGAGTACC 1020  
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DB 1021 TGGGCAAAAGGTGGCCGTGAAGATATCAAGTGTGATGACAGCCAGGCTTCTCTGG 1080  
QY 1081 ACGAGACGCGGCTATGACGAAGATGCAACACGAAACCTGTGCTCTCGGGCGTGA 1140  
DB 1081 ACGAGACGCGGCTATGACGAAGATGCAACACGAAACCTGTGCTCTCGGGCGTGA 1140  
QY 1141 TCCTGACACAGGGGCTGTACATTTGTCAATGAGACAGTGAAGGGCAACCTGTGAACT 1200  
DB 1141 TCCTGACACAGGGGCTGTACATTTGTCAATGAGACAGTGAAGGGCAACCTGTGAACT 1200  
QY 1201 TTTCTGCGAGCCCGGGGCTGAGCCCTGTGAAACACCGCTACGCTCTGCAAGTTTCTGTC 1260  
DB 1201 TTTCTGCGAGCCCGGGGCTGAGCCCTGTGAAACACCGCTACGCTCTGCAAGTTTCTGTC 1260  
QY 1261 ACGTGGCCGAGGGCATGTGAGTACCTGAGACCAAGACTGTGTGACCGGCACTGGGCG 1320  
DB 1261 ACGTGGCCGAGGGCATGTGAGTACCTGAGACCAAGACTGTGTGACCGGCACTGGGCG 1320  
QY 1321 CCGCGCAATCTGTGTCACAGAGACCTGTGTGCGCAAGGCTGTGACCGGCACTGGGCG 1380  
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QY 1381 AAGCCGAGCGGAAGGGGCTAGACTCAAGCGGCTGCCCCGTCAAGTGAAGCGGCGCGAG 1440  
DB 1381 AAGCCGAGCGGAAGGGGCTAGACTCAAGCGGCTGCCCCGTCAAGTGAAGCGGCGCGAG 1440  
QY 1441 CTCTCAAAACAGGGAAGTTTCAACGCAAGTGTGTGAGTTTGGGGTGTGCTCT 1500  
DB 1441 CTCTCAAAACAGGGAAGTTTCAACGCAAGTGTGTGAGTTTGGGGTGTGCTCT 1500  
QY 1501 GGGAGGCTTCTCAATATGAGAGGCTCCGTACCTTAAATATCTCACTGAAAGAGGTGTGG 1560  
DB 1501 GGGAGGCTTCTCAATATGAGAGGCTCCGTACCTTAAATATCTCACTGAAAGAGGTGTGG 1560  
QY 1561 AGGCGGTGAGAGAGGGGTACCGCATGGAACCCCGGAGGCTGTCCAGGCGCCGTCAGC 1620  
DB 1561 AGGCGGTGAGAGAGGGGTACCGCATGGAACCCCGGAGGCTGTCCAGGCGCCGTCAGC 1620

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QY      1621  TCCTCATGAGACAGCTGCTGGGAGGCGAGAGCCGCCCGCGGACACCTTCCGCAAACTGG  1680
Db      1621  TCCTCATGAGACAGCTGCTGGGAGGCGAGAGCCGCCCGCGGACACCTTCCGCAAACTGG  1680
QY      1621  TCCTCATGAGACAGCTGCTGGGAGGCGAGAGCCGCCCGCGGACACCTTCCGCAAACTGG  1680
Db      1681  CCGAAGAGCTGGCCCCGGAGGCTACGACAGTGCAGGTGGCCCCAGCTCCGCTCAGGGCAGG  1740
QY      1741  ACGGCGACGGGTCCACCTCGCGCCCGGAAGCCAGAGCCCTGACCCCAACCCTGGGGCCCT  1800
Db      1741  ACGGCGACGGGTCCACCTCGCGCCCGGAAGCCAGAGCCCTGACCCCAACCCTGGGGCCCT  1800
QY      1801  TGGCCCCAGAGAGACCGAGAGAGTGCAGAGTGCAGGCGTGGGGGCGACTGACACAGGCCCAAG  1860
Db      1801  TGGCCCCAGAGAGACCGAGAGAGTGCAGAGTGCAGGCGTGGGGGCGACTGACACAGGCCCAAG  1860
QY      1861  AGGGTCCAGGCGGGGCAAGTATCCTCTGTGTGCCCCAGACAGCAGGGGCTGGCCACAGTAGG  1920
Db      1861  AGGGTCCAGGCGGGGCAAGTATCCTCTGTGTGCCCCAGACAGCAGGGGCTGGCCACAGTAGG  1920
QY      1921  GGGCTGTGGGGGGGGCCCGTGGAGACACCCCAAGACTGTGGGAAGGATGATCGCCCAATAAGACG  1980
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QY      1981  ATTCTAAGACTCTAATAAAA 2000
Db      1981  ATTCTAAGACTCTAATAAAA 2000

RESULT 3
PCT-US95-05008-1
: Sequence 1, Application PC/RUS9505008
: GENERAL INFORMATION:
:   APPLICANT:  Sugan, Inc.
:   APPLICANT:  515 Galveston Drive
:   APPLICANT:  Redwood City, California 94063-4720
:   APPLICANT:  United States of America
:   APPLICANT:  Wissenschaften E.V.
:   APPLICANT:  Hofgarten Str. 2
:   APPLICANT:  Munchen 80539
:   APPLICANT:  Germany
:   TITLE OF INVENTION:  Novel Megakaryocytic Protein Tyrosine
:   TITLE OF INVENTION:  Kinases
:   NUMBER OF SEQUENCES:  21
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE:  Pennie & Edmonds
:     STREET:    1155 Avenue of The Americas
:     CITY:      New York
:     STATE:     New York
:     COUNTRY:   U.S.A.
:     ZIP:       10036
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE:  Floppy disk
:     COMPUTER:     IBM PC compatible
:     OPERATING SYSTEM:  PC-DOS/MS-DOS
:     SOFTWARE:      Patent Release #1.0, Version #1.25
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER:  PCT/US95/05008
:     FILING DATE:       24-Apr-1995
:   CLASSIFICATION:
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER:  US 08/232,545
:       FILING DATE:       22-Apr-1994
:   CLASSIFICATION:
:     ATTORNEY/AGENT INFORMATION:
:       NAME:  Coruzzi, Laura A.
:       REGISTRATION NUMBER:  30,742
:       REFERENCE/DOCKET NUMBER:  7683-074
:     TELECOMMUNICATION INFORMATION:
:       TELEPHONE:  (212)790-9090
:       TELEFAX:   (212)869-9741
:       TELEX:     66141 PENNIE

```

[illegible]

QY 901 GGACCAAGTCGGCCGAGGAGGAGCTGGCCAGGGCGGGCTGGTTACTGAACTGCAGCAT 960  
 Db 901 GGACCAAGTCGGCCGAGGAGGAGCTGGCCAGGGCGGGCTGGTTACTGAACTGCAGCAT 960  
 QY 961 TGACATTTGGGAGCAGATGAGAGGAGGAGGAGTTGGAGCTGCTGACAGGAGTACC 1020  
 Db 961 TGACATTTGGGAGCAGATGAGAGGAGGAGGAGTTGGAGCTGCTGACAGGAGTACC 1020  
 QY 1021 TGGGGCAAAAGTGGCCGTGAGAAATATCAAGTGTGATGACAGCCAGCCCTTCTG 1080  
 Db 1021 TGGGGCAAAAGTGGCCGTGAGAAATATCAAGTGTGATGACAGCCAGCCCTTCTG 1080  
 QY 1081 ACAGAGAGCGGCTGATGACAGAGATGACACAGAGAACTGTGCGCTCTCTGGGCGTGA 1140  
 Db 1081 ACAGAGAGCGGCTGATGACAGAGATGACACAGAGAACTGTGCGCTCTCTGGGCGTGA 1140  
 QY 1141 TCGTGCACCGGGGCTGTATATGTCATGAGACAGCGTGAAGGCAAGGCGACCTGTA 1200  
 Db 1141 TCGTGCACCGGGGCTGTATATGTCATGAGACAGCGTGAAGGCGACCTGTA 1200  
 QY 1201 TTCTGGGACCGGGGCTGAGCCCTGTAACACCGCTGACCTCTGAGTTTCTGTCG 1260  
 Db 1201 TTCTGGGACCGGGGCTGAGCCCTGTAACACCGCTGACCTCTGAGTTTCTGTCG 1260  
 QY 1261 ACGTGGCCGAGGAGCATGAGTACCTGGAGAGCAAGACTTGTGACACCGGACCTGGCCG 1320  
 Db 1261 ACGTGGCCGAGGAGCATGAGTACCTGGAGAGCAAGACTTGTGACACCGGACCTGGCCG 1320  
 QY 1321 CCGGCAACATCTCTGTCTCAGAGGAGCTGTGGCCAAAGTCTGAGGAGCTTTGGCCCTCA 1380  
 Db 1321 CCGGCAACATCTCTGTCTCAGAGGAGCTGTGGCCAAAGTCTGAGGAGCTTTGGCCCTCA 1380  
 QY 1381 AACCCGAGCGGAGGAGGCTGAGTCAAGCCGGCTGCGCTCAAGTGAAGGCGCCGAGG 1440  
 Db 1381 AACCCGAGCGGAGGAGGCTGAGTCAAGCCGGCTGCGCTCAAGTGAAGGCGCCGAGG 1440  
 QY 1441 CTCTCAAAACAGGGAAGTTTACCAGCAAGTCTGAGTGTGAGTGTGAGGCTGCTCT 1500  
 Db 1441 CTCTCAAAACAGGGAAGTTTACCAGCAAGTCTGAGTGTGAGTGTGAGGCTGCTCT 1500  
 QY 1501 GGGAGGCTCTCTATATGAGAGGAGCTGCTGACCTTAAATGTCACTGAAAGAGGTGCG 1560  
 Db 1501 GGGAGGCTCTCTATATGAGAGGAGCTGCTGACCTTAAATGTCACTGAAAGAGGTGCG 1560  
 QY 1561 AGGCGGTGAGAGGAGGAGTACCGATGAGAACCCCGGAGGCTGTCCAGGCGCCGTGACG 1620  
 Db 1561 AGGCGGTGAGAGGAGGAGTACCGATGAGAACCCCGGAGGCTGTCCAGGCGCCGTGACG 1620  
 QY 1621 TCCTCATGAGCAGCTGCTGGAGGAGAGCCCGCCGCGCCACCTTCCGCAAACTGG 1680  
 Db 1621 TCCTCATGAGCAGCTGCTGGAGGAGAGCCCGCCGCGCCACCTTCCGCAAACTGG 1680  
 QY 1681 CCGAGAAAGTGGCCCGGAGCTACGCAAGTGCAGGTGCCCCAGCCTCGTCTCAGGCGAGG 1740  
 Db 1681 CCGAGAAAGTGGCCCGGAGCTACGCAAGTGCAGGTGCCCCAGCCTCGTCTCAGGCGAGG 1740  
 QY 1741 AGGCGAGGCTGCTGCTGCGCCGAGAGGAGGAGGCGCTGACCCACCGGCTGGGCGCT 1800  
 Db 1741 AGGCGAGGCTGCTGCTGCGCCGAGAGGAGGAGGCGCTGACCCACCGGCTGGGCGCT 1800  
 QY 1801 TGGCCCGAGAGAGCGAGAGAGTGCAGGCTGTGGGCGCATGACCAAGGCGCCAAAG 1860  
 Db 1801 TGGCCCGAGAGAGCGAGAGAGTGCAGGCTGTGGGCGCATGACCAAGGCGCCAAAG 1860  
 QY 1861 AGGCTCCAGGCGGAGAGTATCTCTGCTGCTGCGCCACAGAGGAGGCTGCGCCAGT 1920  
 Db 1861 AGGCTCCAGGCGGAGAGTATCTCTGCTGCTGCGCCACAGAGGAGGCTGCGCCAGT 1920  
 QY 1921 GGGCTTGGGCGGCGGAGAGCCGAGAGCTGCGAGAGGATGATCGCCGATTAAGACGG 1980  
 Db 1921 GGGCTTGGGCGGCGGAGAGCCGAGAGCTGCGAGAGGATGATCGCCGATTAAGACGG 1980  
 QY 1981 ATTCTAAGAGACTCTAAAAA 2000

Db 1981 ATTCTAAGAGACTCTAAAAA 2000  
 RESULT 4  
 US-08-876-882-1  
 : Sequence 1, Application US/08876882  
 : Patent No. 5981201  
 : GENERAL INFORMATION:  
 : APPLICANT: Abraham, Hava  
 : APPLICANT: Groopman, Jerome E.  
 : TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT  
 : NUMBER OF SEQUENCES: 9  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Hamilton, Brook, Smith & Reynolds P.C.  
 : STREET: Two Militia Drive  
 : CITY: Lexington  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02173-4799  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: Windows  
 : SOFTWARE: FastSeq for Windows Version 2.0b  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/876,882  
 : FILING DATE: 16-JUN-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 60/035,228  
 : FILING DATE: 08-JAN-1997  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Doreen, Hogle M.  
 : REGISTRATION NUMBER: 36,361  
 : REFERENCE/DOCKET NUMBER: NED97-01pa  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 781-861-6240  
 : TELEFAX: 781-861-9540  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1987 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : US-08-876-882-1  
 Query Match 95.5%; Score 1909.8; DB 2; Length 1987;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1973; Conservative 0; Mismatches 7; Indels 9; Gaps 5;  
 QY 1 CTCGCTCAAGATTGTGAGCGCGGAGCCGCTCGGGGTGTGACAGCGGCTGCGGAGGCC 60  
 Db 8 CTCGCTCAAGATTGTGAGCGCGGAGCCGCTCGGGGTGTGACAGCGGCTGCGGAGGCC 67  
 QY 61 TCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
 Db 68 TCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 127  
 QY 121 AGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
 Db 128 AGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 187  
 QY 181 GGCATTTCCAGAGGTCGCCAGACTGTGACACTTGTGCTGAGTGTGCTTCACTGCTGAG 240  
 Db 188 GGCATTTCCAGAGGTCGCCAGACTGTGACACTTGTGCTGAGTGTGCTTCACTGCTGAG 247  
 QY 241 TTTTCCCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 Db 248 TTTTCCCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 305

301 GCTGATTCTCTGAGAGACTTCCCGGGTGTAGACCCCGCTTCTCTCCGAGCTTGGCAC 360  
 306 GCTGATTCTCTGAGAGACTTCCCGGGTGTAGACCCCGCTTCTCTCCGAGCTTGGCAC 365  
 361 CCCCTCCCGTCTCAGCCAGAGATGCAACAGAGCGCTGGGCCCCGGGACCCAGTGTATCA 420  
 366 CCCCTCCCGTCTCAGCCAGAGATGCAACAGAGCGCTGGGCCCCGGGACCCAGTGTATCA 425  
 421 CCAATGCGAGCACACCCCGCCCAAGAGAGGAGCTGGCTTCCGCAAGGGCGAGCTGG 480  
 426 CCAATGCGAGCACACCCCGCCCAAGAGAGGAGCTGGCTTCCGCAAGGGCGAGCTGG 485  
 481 TCACCATCTCTGAGAGCTTCCGCAAGAGAGCTGGTACCGGTCAAGACCAACACAGTGG 540  
 486 TCACCATCTCTGAGAGCTTCCGCAAGAGAGCTGGTACCGGTCAAGACCAACACAGTGG 545  
 541 GACAGAGAGGAGTGTGGAGCTGGGCGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
 546 GACAGAGAGGAGTGTGGAGCTGGGCGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 605  
 601 CCAAGCTCAGCTCTATGCGCTGTTCACAGGGAGAGATCTCGGGCCAGAGAGGCTGTCAAC 660  
 606 CCAAGCTCAGCTCTATGCGCTGTTCACAGGGAGAGATCTCGGGCCAGAGAGGCTGTCAAC 665  
 661 AGCTGACAGCTTCCGAGAGATGGGCTGTCTCTGCTGGGAGTCCGCGCCACCCCGCG 720  
 666 AGCTGACAGCTTCCGAGAGATGGGCTGTCTCTGCTGGGAGTCCGCGCCACCCCGCG 725  
 721 ACTAGCTCTGTGCTGTGAGCTTTGGCGGAGCTGATCACTACAGGCGCTGTCAACCGG 780  
 726 ACTAGCTCTGTGCTGTGAGCTTTGGCGGAGCTGATCACTACAGGCGCTGTCAACCGG 785  
 781 ACGGCGACCTCACAATGATGAGGCGGTGTCTCTGCAACCTCATGACATGATGTGAGC 840  
 786 ACGGCGACCTCACAATGATGAGGCGGTGTCTCTGCAACCTCATGACATGATGTGAGC 845  
 841 ATTACAGAGAGAGAGAGGCGCTATCTGACCAACCTGCTGAGACCAAGCGAGAAACAG 900  
 846 ATTACAGAGAGAGAGAGGCGCTATCTGACCAACCTGCTGAGACCAAGCGAGAAACAG 905  
 901 GGACCAAGTGGCGCGAGAGAGAGTGGCGGCGGCGGTGTACTGAACCTGACAGCAT 960  
 906 GGACCAAGTGGCGCGAGAGAGAGTGGCGGCGGCGGTGTACTGAACCTGACAGCAT 965  
 961 TGACATTGGGAGACACAGATCGAGAGAGAGAGTTTGGAGCTGTCTCTGAGGGTGAATAC 1020  
 966 TGACATTGGGAGACACAGATCGAGAGAGAGAGTTTGGAGCTGTCTCTGAGGGTGAATAC 1025  
 1021 TGGGCGCAAAAGTGGCGCTGAAAGATATCAAGTGTGATGTGACAGCCCAAGGCTTCC 1080  
 1026 TGGGCGCAAAAGTGGCGCTGAAAGATATCAAGTGTGATGTGACAGCCCAAGGCTTCC 1085  
 1081 ACGAGAGCGCGCTGTATGAGAGAGATGCAACAGAGAGAGAGTGGTGTCTCTGAGGGCTGA 1140  
 1086 ACGAGAGCGCGCTGTATGAGAGAGATGCAACAGAGAGAGAGTGGTGTCTCTGAGGGCTGA 1145  
 1141 TCTGCGACAGAGGCGCTGTATGAGAGAGATGCAACAGAGAGAGAGTGGTGTCTCTGAGGGCTGA 1200  
 1146 TCTGCGACAGAGGCGCTGTATGAGAGAGATGCAACAGAGAGAGAGTGGTGTCTCTGAGGGCTGA 1205  
 1201 TTTCTGCGAGAGCGGCGCTGTATGAGAGAGATGCAACAGAGAGAGAGTGGTGTCTCTGAGGGCTGA 1260  
 1206 TTTCTGCGAGAGCGGCGCTGTATGAGAGAGATGCAACAGAGAGAGAGTGGTGTCTCTGAGGGCTGA 1265  
 1261 ACGTGGCGAGAGGAGATGAGTACCTGGAGAGAGAGAGTGGTGTCTCTGAGGGCGAG 1320  
 1266 ACGTGGCGAGAGGAGATGAGTACCTGGAGAGAGAGAGTGGTGTCTCTGAGGGCGAG 1325  
 1321 CCGGCAACATCTGTGCTCAGAGAGAGCTGTGGGCGCAAGGTGACAGCACTTTGGCGTGGCA 1380  
 1326 CCGGCAACATCTGTGCTCAGAGAGAGCTGTGGGCGCAAGGTGACAGCACTTTGGCGTGGCA 1385  
 1381 AAGCGAGAGGAGAGGCGCTAGACTCAAGCGGCTGCCGCTCAAGTGAAGCGGCGCGGAGG 1440

1386 AAGCGAGAGGAGAGGCTGAGACTCAAGCGGCTGCCGTCAAGTGAAGAGGAGGCGCGAGG 1445  
 1441 CTCTCAACACAGGAGATTCACACAGAGTCCGATGTCTGAGATTTTGGGTGTCTCT 1500  
 1446 CTCTCAACACAGG---GTTACACAGCAAGTGGATGTCTGAGATTTTGGGTGTCTCT 1502  
 1501 GGGAGCTCTCTCATATGAGAGCGGCTCCGATACCTTAAATGTCATCTGAAGAGTGTGG 1560  
 1503 GGGAGCTCTCTCATATGAGAGCGGCTCCGATACCTTAAATGTCATCTGAAGAGTGTGG 1562  
 1561 AGGCGGTGAGAGAGGAGTACCGCATGGAACCCCGGAGGCGTGTCCAGGCGCGGAGAG 1620  
 1563 AGGCGGTGAGAGAGGAGTACCGCATGGAACCCCGGAGGCGTGTCCAGGCGCGGAGAG 1622  
 1621 TCCTCATGAGAGAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
 1623 TCCTCATGAGAGAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1681  
 1681 CCGAGAGAGTGGCGCGGAGAGTACGCAAGTGTGAGTGTCCAGAGCTTCTCTAGAGGAG 1740  
 1682 CCGAGAGAGTGGCGCGGAGAGTACGCAAGTGTGAGTGTCCAGAGCTTCTCTAGAGGAG 1741  
 1741 AGCGGAGAGAGTGTCCAGAGTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
 1742 AGCGGAGAGAGTGTCCAGAGTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1798  
 1801 TGGCGCGAG 1860  
 1799 TGGCGCGAG 1858  
 1861 AGGCTCAG 1920  
 1859 AGGCTCAG 1918  
 1921 GGGCTGAG 1980  
 1919 GGGCTGAG 1978  
 1981 ATTCTAAGG 1989  
 1979 ATTCTAAGG 1987

RESULT 5  
 US-09-315-928-1  
 ; Sequence 1, Application US/09315928  
 ; Patent No. 6368796  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AVTAM, Hava  
 ; APPLICANT: Groopman, Jerome E.  
 ; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF  
 ; FILE REFERENCE: MED97-01PAZ  
 ; CURRENT FILING DATE: US/09/315,928  
 ; PRIOR FILING DATE: 1999-05-20  
 ; PRIOR APPLICATION NUMBER: US 08/876,882  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/035,228  
 ; PRIOR FILING DATE: 1997-01-08  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1987  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (263)...(1846)  
 ; US-09-315-928-1

Query Match 95.5%; Score 1909.8; DB 4; Length 1987;  
 Best Local Similarity 99.2%; Pred. No. 0;

Matches 1973; Conservative 0; Mismatches 7; Indels 9; Gaps 5;

OY	1	CTCGCTCCAAAGTTGTGTGACAGCCGGAGACCCGCTCTCGGGGTGTGCAAGCCGGCTCGCGAGGCC	60
Db	8	CTCGGTCCAAAGTTGTGTGACAGCCGGAGACCCGCTCTCGGGGTGTGCAAGCCGGCTCGCGAGGCC	67
OY	61	TCCTGGGGGGGGGGCGGGGGGGCGCTCGGGGGGGGGCCCTCGAGACAGAAAAAGGAAGAAC	120
Db	68	TCCTGGGGGGGGGGGGGGGGGGGGCGGCTCTGGGGGGGGCCCCCTGAGACAGAAAAAGGAAGAAC	127
OY	121	AGGCTGGGTCCAGTGGACACCAAGCTCCCTACCTCTCTGTGCCAGCGCCCTGGGCTGTGACA	180
Db	128	AGGCTGGGTCCAGTGGACACCAAGCTCCCTACCTCTCTGTGCCAGCGCCCTGGGCTGTGACA	187
OY	181	GGCCATTCCCAAGCGTCCCGGACGCTGTGACACTGTGTCTAGTGTGCTCTCACCCTGGCTAG	240
Db	188	GGCCATTCCCAAGCGTCCCGGACGCTGTGACACTGTGTCTAGTGTGCTCTCACCCTGGCTAG	247
OY	241	TTTCCCTGTGGGGGGGGCGATGGCGGGGGGAGGCTCTCTGATTTCCGTGGGGGCAATTTCAG	300
Db	248	TTTCC - TCTGGGGGGCGATGGGGGGGAGGCTCTCTGTGTTTCTGTGGGGGCAATTTCAG	305
OY	301	GCTGTGATTTCTGTGAGAACTTCCCGGGGTGAGCCCGCTTCTCTCGAGCTTGACAC	360
Db	306	GCTGTGATTTCTGTGAGAACTTCCCGGGGTGAGCCCGCTTCTCTCGAGCTTGACAC	365
OY	361	CCCCCCCCGTCCACCCAGAGATGGCCAAAGAGAGCGCTGGGGCCCCGGGGACCCAGTTATCA	420
Db	366	CCCCCCCCGTCTCAGCCAGCAAGATGCCAACAGAGCGTGGGGCCCCGGGGACCCAGTTATCA	425
OY	421	CCAAATGCGAGACACCCCGCCAAAGCCAGGGGAGCTGGCTTCCGCAAGGGCGACGTTGG	480
Db	426	CCAAATGCGAGACACCCCGCCAAAGCCAGGGGAGCTGGCTTCCGCAAGGGCGAGCTGG	485
OY	481	TCACCATCTTGAAGGCGTGCAGAAACAGAGCTGTACCGGGTCAAGACACACACCACTG	540
Db	486	TCACCATCTTGAAGGCGTGCAGAAACAGAGCTGTACCGGGTCAAGACACACCACTG	545
OY	541	GACAGGAGGGGCTGTGTGACAGCTGGGGGCGTCTGCGGAGACGGGAGGAGCCCTCTCCGAGACC	600
Db	546	GACAGGAGGGGCTGTGTGACAGCTGGGGGCGTCTGCGGAGACGGGAGGAGCCCTCTCCGAGACC	605
OY	601	CCAAAGCTAGCTCATGTCCGTTGTTCCACGGGAGATTTGCGGGCCAGGAGCTGTCCAGC	660
Db	606	CCAAAGCTAGCTCATGTCCGTTGTTCCACGGGAGATTTGCGGGCCAGGAGCTGTCCAGC	665
OY	661	AGCTGCAGCTCTCCGAGAGTGGGCTTCTCTGTGTCGGGAGTCCGGCGGCCACCCCGGCG	720
Db	666	AGCTGCAGCTCTCCGAGAGTGGGCTTCTCTGTGTCGGGAGTCCGGCGGCCACCCCGGCG	725
OY	721	ACTACGTCCTGTGCGTGTGAGCTTTTGGCCGACGTCATCCACTACCGGTGCTGCACCGG	780
Db	726	ACTACGTCCTGTGCGTGTGAGCTTTTGGCCGACGTCATCCACTACCGGTGCTGCACCGG	785
OY	781	ACGGGCACTTCACAAATGATGATGAGGCGGTCTTCTGTGAACCTATGACATGATGTGTGAGC	840
Db	786	ACGGGCACTTCACAAATGATGATGAGGCGGTCTTCTGTGAACCTATGACATGATGTGTGAGC	845
OY	841	ATTACAGCAAGACAAAGGGCGCTATTCTGCACCAAGCTGTGTGAGACCAAAAGGGAGAACAG	900
Db	846	ATTACAGCAAGACAAAGGGCGCTATTCTGCACCAAGCTGTGTGAGACCAAAAGGGAGAACAG	905
OY	901	GGACCAAGTCCGGCCGAGAGAGAGCTGGCCAGGGCGGGCTGGTTACTGAACCTGCAGCAATT	960
Db	906	GGACCAAGTCCGGCCGAGAGAGAGCTGGCCAGGGCGGGCTGGTTACTGAACCTGCAGCAATT	965
OY	961	TGACATTGTGGAGACAGATTCGAGAGAGGAGATTTGAGCTGTCTCGAGGGGTGATATCC	1020
Db	966	TGACATTGTGGAGACAGATTCGAGAGAGGAGATTTGAGCTGTCTCGAGGGGTGATATCC	1025
OY	1021	TGGGGCAAAAGGTTGGCTGAAGAAATATCAAGTGTGATGTGACAGACCCAGGCTTTCCTGG	1080
Db	1026	TGGGGCAAAAGTGTGGCTGTGAAGAAATATCAAGTGTGATGTGACAGACCCAGGCTTTCCTGG	1085

OY	1081	ACGAGAGCGCGCGTATGACGAAGATGCAACACGAGAACTGCTGCTCTCGGCGTGA	1140
Db	1086	ACGAGAGCGCGCGTATGACGAAGATGCAACACGAGAACTGCTGCTCTCGGCGTGA	1145
OY	1141	TCGAGACACGAGGGCGTGTACATTTCATGTGGAGCAGTGAAGGCAACCTGGTGAAC	1200
Db	1146	TCCTGACACGAGGGCGTGTACATTTCATGTAGAGCACGTGAGCAAGGGCAACCTGGTGAAC	1205
OY	1201	TTTCTGCGGACCCGGGGTGTGAGCCCTCGTAGAACACCGCTCAAGCTCTGCAGTTTCTCTGC	1260
Db	1206	TTTCTGCGGACCCGGGGTGTGAGCCCTCGTAGAACACCGCTCAAGCTCTGCAGTTTCTCTGC	1265
OY	1261	ACGTGCGCGAGGGCATGTAGTACTGTGGAGAGCAAGAACTTGTGACCGGACCTGGCCG	1320
Db	1266	ACGTGCGCGAGGGCATGTAGTACTGTGGAGAGCAAGAACTTGTGACCGGACCTGGCCG	1325
OY	1321	CCGCGCAACATCTGTCTGACAGAGAACCTGGTGGCGCAAGTGCAGGACCTTGGCTGGCCA	1380
Db	1326	CCGCGCAACATCTGTCTGACAGAGAACCTGGTGGCGCAAGTGCAGGACCTTGGCTGGCCA	1385
OY	1381	AAGCGGAGCGGAAAGGGGCTAGACTCAAGCCGGCTGCCCTGTCAAGTGAAGCGGCCGACAG	1440
Db	1386	AAGCGGAGCGGAAAGGGGCTAGACTCAAGCCGGCTGCCCTGTCAAGTGAAGCGGCCGACAG	1445
OY	1441	CTCTCAAAACACGGGAAATTACACGACGAAAGTCGGATGTCTGGAGTTTGGGGTGTCTCT	1500
Db	1446	CTCTCAAAACACGG--GTTCAACCAGCAAGTCGGATGTCTGGAGTTTGGGGTGTCTCT	1502
OY	1501	GGGAGGTCCTTCTCATATGGAACGGGCTCGTACCCCTAAATGTCACTGAAGAGGTGTCGG	1560
Db	1503	GGGAGGTCCTTCTCATATGGAACGGGCTCGTACCCCTAAATGTCACTGAAGAGGTGTCGG	1562
OY	1561	AGGCGTGTGAGAAAGGGGTACCGCATGTGGAACCCCGGAGGGCTGTCCAGGGCCCTGTGCAG	1620
Db	1563	AGGCGTGTGAGAAAGGGGTACCGCATGTGGAACCCCGGAGGGCTGTCCAGGGCCCTGTGCAG	1622
OY	1621	TCTCTATGAGCAGCTGCTGGGAGGCAAGACCCCGCGCCGACACCTTCGCGCAACTGG	1680
Db	1623	TCTCTATGAGCAGCTGCTGGGAGGCAAG--CCGCGCCCGCGCCACCTTCGCGCAACTGG	1681
OY	1681	CCGAGAGCTGTGGCCCGGGAGGTACGAGTGAAGTGTGCCAGGCTTCGTCTCAAGGGGAGG	1740
Db	1682	CCGAGAGCTGTGGCCCGGGAGGTACGAGTGAAGTGTGCCAGGCTTCGTCTCAAGGGGAGG	1741
OY	1741	ACGCGCAGCGGCTCCACCTCGGCCCGGAGCCGAGGAGGCGGCTGTACCCGACCGGCTGGGGGCT	1800
Db	1742	ACGCGCAGCGG--TCCACTCGGCCCGGAGGCCAGGAGGCTGTACCCGACCGG--GGCGCT	1798
OY	1801	TGCGCCCGCAGAGGACCGAGAGAGTGTGAAGTGTGGCGGCTGTGGGGGCACTGACAGGCCACAG	1860
Db	1799	TGCGCCCGCAGAGGACCGAGAGAGTGTGAAGTGTGGCGGCTGTGGGGGCACTGACAGGCCACAG	1858
OY	1861	AGGGTCCAGAGGGGGCAAGTCACTCCTCTGTGGGCCCAAGAGAGGGGGCTGGGGCCAGTAAAG	1920
Db	1859	AGGGTCCAGAGGGGGCAAGTCACTCCTCTGTGGGCCCAAGAGAGGGGGCTGGGGCCAGTAAAG	1918
OY	1921	GGCTCTGTGGGGGCGCGGTGAGACACCCGACAGCTGTGGAAGATGTATGCGCCGATAAAGACG	1980
Db	1919	GGCTCTGTGGGGGCGCGGTGAGACACCCGACAGCTGTGGAAGATGTATGCGCCGATAAAGACG	1978
OY	1981	ATTCTTAAGG 1989	
Db	1979	ATTCTTAAGG 1987	

RESULT 6  
US-08-604-989A-11  
Sequence 11, Application US/08604989A  
Patent No. 5834208  
GENERAL INFORMATION:  
APPLICANT: Sakano, S.  
TITLE OF INVENTION: No. 5834208el Tyrosine Kinase



NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: PastSeq Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/604,989A  
 FILING DATE: February 23, 1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Charles E. Miller  
 REGISTRATION NUMBER: 24,576  
 REFERENCE/DOCKET NUMBER: 1920-026  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864/9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1942 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 ORIGINAL SOURCE:  
 ORGANISM: human  
 STRAIN: UT-7  
 US-08-604-989A-11

Query Match 95.2%; Score 1903.4; DB 2; Length 1942;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1939; Conservative 0; Mismatches 1; Indels 5; Gaps 3;

52 CGGAGGCGCTCTGGGGGGGGGGGGG--GCGGCTGGGGGGGGGGGGGGGAGGAA 109  
 1 CGGAGGCGCTCTGG 60  
 110 CAGGAAGAACAGGCTCGGTCAGTGGACCCAGCTCCCTACCTCTGTGCCAGCGCT 169  
 61 CAGGAAGAACAGGCTCGGTCAGTGGACCCAGCTCCCTACCTCTGTGCCAGCGCT 120  
 170 GGGCTGTGGAGGCGCATTCGCCAGGCTCCCGACTGTGACACACTTGTCTGCTCTC 229  
 121 GGGCTGTGGAGGCGCATTCGCCAGGCTCCCGACTGTGACACACTTGTCTGCTCTC 180  
 230 ACCTGCGTCAGTTTCCCTCTGGGGGGGCGATGGGGGGGGGGGGGGGGGGGGGGGG 289  
 181 ACCTGCGTCAGTTTCCCTCT--GGGGGGGATGGGGGGGGGGGGGGGGGGGGGGGG 239  
 290 GGCATTTACGCGCTGTGATCTGTGTGAGAACTTCCCGGGGTGAGAGCCCGGCTTCTCG 349  
 240 GGCATTTACGCGCTGTGATCTGTGTGAGAACTTCCCGGGGTGAGAGCCCGGCTTCTCG 299  
 350 AGCGTGGACCCCGCTCCCGTCTCAGCCAGATGCAAGAGGCGCTGGGGCCCGGGGAC 359  
 300 AGCGTGGACCCCGCTCCCGTCTCAGCCAGATGCAAGAGGCGCTGGGGCCCGGGGAC 359  
 410 CCAGGTATCACCAATGCGAGACACCGCGCCCAAGGACGAGGAGTGGGCTTCCGAA 469  
 360 CCAGGTATCACCAATGCGAGACACCGCGCCCAAGGACGAGGAGTGGGCTTCCGAA 419  
 470 GGGGAGCTGTACCATCTGTGAGAGCTGTGAGAAAGAGCTGTACCGGTCAACCA 529  
 420 GGGGAGCTGTGTACCATCTGTGAGAGCTGTGAGAAAGAGCTGTGTACCGGTCAACCA 479

530 CCACACAGTGGACAGAGAGGGCTGTGGACCTGGGGGGCTGGGGAGCGGGAGCCCT 589  
 480 CCACACAGTGGACAGAGAGGGCTGTGGACCTGGGGGGCTGGGGAGCGGGAGCCCT 539  
 590 CTCCGAGAGCCCAAGCTACAGCTCATGCCGCTTCCACGGAGAGATTCGGCCAGGA 649  
 540 CTCCGAGAGCCCAAGCTACAGCTCATGCCGCTTCCACGGAGAGATTCGGCCAGGA 599  
 650 GGGCTGTACAGAGCTGACAGCCCTCCGAGAGTGGGCTGTCTGTGGGGAGTCCGCGG 709  
 600 GGGCTGTACAGAGCTGACAGCCCTCCGAGAGTGGGCTGTCTGTGGGGAGTCCGCGG 659  
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 660 CCACCCCGGAGCTACAGCTGTGGCTGACCTTGGCCGCGGAGCATCCACTACCGGT 719  
 770 GCTGACCGGAGCGGAGCTACAGCTGTGGCTGACCTTGGCCGCGGAGCATCCACTACG 829  
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 780 CATGTGTGAGCATTTACAGCAAGAGAGGCGCTATCTGACCAAGCTGTGAGACCAAA 839  
 890 GCGGAAACACGGGAGACCAAGTGGCGGAGGAGAGCTGGCCAGGGGGGCTGTACTGAA 949  
 840 GCGGAAACACGGGAGACCAAGTGGCGGAGGAGAGCTGGCCAGGGGGGCTGTACTGAA 899  
 950 CCTGAGCATTTGACATTTGGAGAGACAGATCGGAGAGGAGAGTTGGAGCTGTCTGCA 1009  
 900 CCTGAGCATTTGACATTTGGAGAGACAGATCGGAGAGGAGAGTTGGAGCTGTCTGCA 959  
 1010 GGGTGTGTACCTGGGGGCAAAAGGTGGCGGTGAAGATATCAAGTGTGTGACAGCCCA 1069  
 960 GGGTGTGTGTACCTGGGGGCAAAAGGTGGCGGTGAAGATATCAAGTGTGTGACAGCCCA 1019  
 1070 GGGCTTCTGTGACAGAGAGGGCGCTCATGACGAAGATGCAACACGAGAACTGTGCTCT 1129  
 1020 GGGCTTCTGTGACAGAGAGGGCGCTCATGACGAAGATGCAACACGAGAACTGTGCTCT 1079  
 1130 CTTGGGCGTGTGACAGAGAGGGCGCTCATGACGAAGATGCAACACGAGAACTGTGCTCT 1189  
 1080 CTTGGGCGTGTGACAGAGAGGGCGCTCATGACGAAGATGCAACACGAGAACTGTGCTCT 1139  
 1190 CTTGGTGTAACTTTTGGCGAGCCGGGGTGCAGCCCTGTGAACACCGCTCACTCTGTGCA 1249  
 1140 CTTGGTGTAACTTTTGGCGAGCCGGGGTGCAGCCCTGTGAACACCGCTCACTCTGTGCA 1199  
 1250 GTTTCCTGTGACAGCTGGCGGAGAGGATGAGTACCTGTGAGAGAGAGAGCTGTGACACG 1309  
 1200 GTTTCCTGTGACAGCTGGCGGAGAGGATGAGTACCTGTGAGAGAGAGAGCTGTGACACG 1259  
 1310 GACCTGGCGCGGCGGCAACATCTGTGTCAAGAGACCTGTGTGCGCAAGTCAAGCACTT 1369  
 1260 GACCTGGCGCGGCGGCAACATCTGTGTCTCAAGAGACCTGTGTGCGCAAGTCAAGCACTT 1319  
 1370 TGGCTGTGGCAAAAGCGGAGGAGGCTGTGACCTCAAGCGGCTGTCAAGTGTGAC 1429  
 1320 TGGCTGTGGCAAAAGCGGAGGAGGCTGTGACCTCAAGCGGCTGTCAAGTGTGAC 1379  
 1430 GGGCGCGGAGGCTGTCAAAACAGGGAAGTTTCAACGAGCAAGTGTGAGTGTGAGTTTGG 1489  
 1380 GGGCGCGGAGGCTGTCAAAACAGGGAAGTTTCAACGAGCAAGTGTGAGTGTGAGTTTGG 1439  
 1490 GGTGTGTGTGTGGAGGCTTCTTCAATATGAGAGGCGCTGTGTCAATATATCACTGAA 1549  
 1440 GGTGTGTGTGTGGAGGCTTCTTCAATATGAGAGGCGCTGTGTCAATATATCACTGAA 1499  
 1550 AGAGTGTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 1609  
 1500 AGAGTGTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 1559  
 1610 CCGGCTGACAGCTTCTCATGTAGAGCTGCTGGAGAGGACAGAGCCCGCGCGGACACCTT 1669



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Db      1560  CCCCCTGACAGTCTCCTCATATGACACACTGCTGGGAGGACAGAGCCGCCCGCGGACACTT 16119
Oy      1670  CCGCCAAACTGGCCCGAGAACTGCGCCCGGAGACTTACGACAGTGCAGGTGCCCCAGGCTTCG 1729
Db      1620  CCCCAGAACTGCGCCGAGAACTGCGCCCGGAGACTTACGACAGTGCAGGTGCCCCAGGCTTCG 1679
Oy      1730  CTCAGGGGAGAGACGCCCGACGGCTCCACTTCGCCCCGAAAGCCAGAGACGCTTACCCACCC 17899
Db      1680  CTCAGGGGAGAGACGCCCGACGGCTCCACTTCGCCCCGAAAGCCAGAGACGCTTACCCACCC 1739
Oy      1790  GGTAGGGGCCCTTGCGCCCGAGAGACCGAGAGATGAGAGATGCGGCGGTGGGGGCACTGAC 1849
Db      1740  GGT--GGCCCTTGCGCCCGAGAGACCGAGAGATGAGAGATGCGGCGGTGGGGGCACTGAC 1797
Oy      1850  CAGGCCCCAAGGAGGCTCCAGGCGGGGCAAGTCACTCTCTGCTGCCCCACAGCAGGSGCTGG 1909
Db      1798  CAGGCCCCAAGGAGGCTCCAGGCGGGGCAAGTCACTCTCTGCTGCCCCACAGCAGGSGCTGG 1857
Oy      1910  CCCACAGTAGGGGGCTCTGCGGGCGCCCGTGGACACCCACAGACTTCGGAAGATGATCGCC 1969
Db      1858  CCCACAGTAGGGGGCTCTGCGGGCGCCCGTGGACACCCACAGACTTCGGAAGATGATCGCC 1917
Oy      1970  GATAAGACGAGTCTTAAGCACTCT 1994
Db      1918  GATTAACACGATTTCTAAGCACTCT 1942

RESULT 7
US-08-604-989A-10
: Sequence 10, Application US/08604989A
: Patent No. 5834208
: GENERAL INFORMATION:
:   APPLICANT: Sakano, S.
:   TITLE OF INVENTION: No. 5834208el Tyrosine Kinase
:   NUMBER OF SEQUENCES: 11
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Pennie & Edmonds LLP
:     STREET: 1155 Avenue of the Americas
:     CITY: New York
:     STATE: New York
:     COUNTRY: USA
:     ZIP: 10036-2711
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Diskette
:   COMPUTER: IBM Compatible
:   OPERATING SYSTEM: DOS
:   SOFTWARE: FastSeq Version 2.0
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/604,989A
:     FILING DATE: February 23, 1996
:     CLASSIFICATION: 435
:     ATTORNEY/AGENT INFORMATION:
:       NAME: Charles F. Miller
:       REGISTRATION NUMBER: 24,576
:       REFERENCE/DOCKET NUMBER: 1920-026
:     TELECOMMUNICATION INFORMATION:
:       TELEPHONE: (212) 790-9090
:       TELEFAX: (212) 869-8864/9741
:     TEXT: 66141 PENNIE
:     INFORMATION FOR SEQ ID NO: 10:
:       SEQUENCE CHARACTERISTICS:
:         LENGTH: 1521 base pairs
:         TYPE: nucleic acid
:         STRANDEDNESS: double
:         TOPOLOGY: linear
:       MOLECULE TYPE: cDNA to mRNA
:       ORIGINAL SOURCE:
:         ORGANISM: human
:         STRAIN: UT-7
:         US-08-604-989A-10
Query Match 76.0%, Score 1519.4, DB 2, Length 1521;

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[illegible]

Db	1021	GAGTACTGAGACAGAAAGACTTGTCACCGGACCTGGCGCCGCCCAACATCTGTGTC	1080
QY	1338	TCAGAGACCTGGTGGCCCAAGGTACGAGCACTTTGGCTGGCCCAAGCCGAGCGAAGGG	1397
Dc	1081	TCAGAGACCTGGTGGCCCAAGGTACGAGCACTTTGGCTGGCCCAAGCCGAGCGAAGGG	1140
QY	1398	CTAGACTCAAGCCGGCGCCGTCACGTGGACGGCGCCGAGGCTCTCAACACGGGAAG	1457
Db	1141	CTAGACTCAAGCCGGCGCTGCCCCGTCAAGTGGACGGCGCCGAGGCTCTCAACACGGGAAG	1200
QY	1458	TTCCACGCAAGTCGTGATGTCGTGGAGTTTGGGGTGTGCTGTGGGAGGTCTTCTCATAT	1517
Db	1201	TTCCACGCAAGTCGTGATGTCGTGGAGTTTGGGGTGTGCTGTGGGAGGTCTTCTCATAT	1260
QY	1518	GGACGGCTCCGTACCTTAATAATGTCACTGAAGAGGTGTGCGAGGGCCGTGGACAGGG	1577
Db	1261	GGACGGCTCCGTACCTTAATAATGTCACTGAAGAGGTGTGCGAGGGCCGTGGAGAAAGGG	1320
QY	1578	TACCGCATGGAAACCCCGGAGGGCTGTCCAGGGCCGCTGGACGTCATAGACAGCTGC	1637
Db	1321	TACCGCATGGAAACCCCGGAGGGCTGTCCAGGGCCGCTGGACGTCATAGACAGCTGC	1380
QY	1638	TGGGAGGCGAGAGCCCGCGCCGCGCCACACCTTCGCGAAACTGGCCGAGAAAGCTGGCCGG	1697
Db	1381	TGGGAGGCGAGAGCCCGCGCCGCGCCACACCTTCGCGAAACTGGCCGAGAAAGCTGGCCGG	1440
QY	1698	GAGCTACGACGATGAGTGGCCCCAGCCTTCGCTGTCAAGGACGACGCCGAGCGCTCCACC	1757
Db	1441	GAGCTACGACGATGAGTGGCCCCAGCCTTCGCTGTCAAGGACGACGCCGAGCGCTCCACC	1500
QY	1758	TTCGCCCGGAGCCGAGAGCC 1778	
Db	1501	TTCGCCCGGAGCCGAGAGCC 1521	
RESULT 8			
US-08-604-989A-9			
Sequence 9, Application US/08604989A			
Patent No. 5834208			
GENERAL INFORMATION:			
APPLICANT: Sakano, S.			
TITLE OF INVENTION: No. 5834208el Tyrosine Kinase			
NUMBER OF SEQUENCES: 11			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Pennie & Edmonds LLP			
STREET: 1155 Avenue of the Americas			
CITY: New York			
STATE: New York			
COUNTRY: USA			
ZIP: 10036-2711			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Diskette			
COMPUTER: IBM Compatible			
OPERATING SYSTEM: DOS			
SOFTWARE: FASTSEQ Version 2.0			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/604,989A			
FILING DATE: February 23, 1996			
CLASSIFICATION: 435			
ATTORNEY/AGENT INFORMATION:			
NAME: Charles E. Miller			
REGISTRATION NUMBER: 24,576			
REFERENCE/DOCKET NUMBER: 1920-026			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (212) 790-9090			
TELEFAX: (212) 869-8864/9741			
TELEX: 66141 PENNIE			
INFORMATION FOR SEQ ID NO: 9:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1398 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: double			
TOPOLOGY: linear			

:	MOLECULE TYPE:	cdna	to	mRNA	
:	ORIGINAL SOURCE:				
:	ORGANISM:	human			
:	STRAIN:	UT-7			
:	US-08-604-989A-9				
	Query Match	69.9%	Score 1398:	DB 2:	Length 1398:
	Best Local Similarity	100.0%	Pred. No. 4e-275:		
	Matches 1398:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
OY	381	ATGCCAACGAGAGCGCTGGGCCCCGGGACCCAGTGTATCACAAATGCGAGCACACCCGC	440		
DB	1	ATGCCAACGAGAGCGCTGGGCCCCGGGACCCAGTGTATCACAAATGCGAGCACACCCGC	60		
OY	441	CCCAAGCCAGGGGAGCTGGCTTCCGCAAGGGGACGTGTCACCATCTCTGGAGGCTTC	500		
DB	61	CCCAAGCCAGGGGAGCTGGCTTCCGCAAGGGGACGTGTCACCATCTCTGGAGGCTTC	120		
OY	501	GAGAACAAAGAGCTGTACCGGGTCACACACACAGTGGAGACGAGGGGGCTGTGGCA	560		
DB	121	GAGAACAAAGAGCTGTACCGGGTCACACACACAGTGGAGACGAGGGGGCTGTGGCA	180		
OY	561	GCTTGGGGCGCTGCGGGGAGGGGAGCCCTCTCCGACAGACCCCAAGCTCACCTCATGCG	620		
DB	181	GCTTGGGGCGCTGCGGGGAGGGGAGCCCTCTCCGACAGACCCCAAGCTCACCTCATGCG	240		
OY	621	TGCTTCCACGGGAAGATCTGGGGCCAGAGGCTGTCCAGACGTGCAGCCTCCGAGGAT	680		
DB	241	TGCTTCCACGGGAAGATCTGGGGCCAGAGGCTGTCCAGACGTGCAGCCTCCGAGGAT	300		
OY	681	GGGCTGTTCCTGGTGGGGGAGTCCGGCGCCACCCGGGCACTACGTCTGTGGTGGC	740		
DB	301	GGGCTGTTCCTGGTGGGGGAGTCCGGCGCCACCCGGGCACTACGTCTGTGGTGGC	360		
OY	741	TTTGGCCGCGACGTATCATCTACCGGCTGCTGCACGCGACGGCCACCTCACAAATGAT	800		
DB	361	TTTGGCCGCGACGTATCATCTACCGGCTGCTGCACGCGACGGCCACCTCACAAATGAT	420		
OY	801	GAGGCGCTGTTCTTCTSCAACCTTCATGACATGTTGAGCATTTACAGCAAGAGACGGC	860		
DB	421	GAGGCGCTGTTCTTCTSCAACCTTCATGACATGTTGAGCATTTACAGCAAGAGACGGC	480		
OY	861	GCTATCTGACCAAGCTGTGTAGACCAAAACGGGAAACACGGGACCAAGTGGCCGAGAG	920		
DB	481	GCTATCTGACCAAGCTGTGTAGACCAAAACGGGAAACACGGGACCAAGTGGCCGAGAG	540		
OY	921	GAGTGGCCAGGGGGGCTGGTACTCAACCTGAGCATTTGACATTGGGAGCACATATC	980		
DB	541	GAGTGGCCAGGGGGGCTGGTACTCAACCTGAGCATTTGACATTGGGAGCACATATC	600		
OY	981	GGAGAGGAGAGATTGGAGCTGTCTCAGGGTGAATACCTGGGGCAAAAGTGGCCGTG	1040		
DB	601	GGAGAGGAGAGATTGGAGCTGTCTCAGGGTGAATACCTGGGGCAAAAGTGGCCGTG	660		
OY	1041	AAGAAATATCAAGTGTGATGTGACAGCCGAGGCTTCTGGAACGAGAGGGCCGTATGAG	1100		
DB	661	AAGAAATATCAAGTGTGATGTGACAGCCGAGGCTTCTGGAACGAGAGGGCCGTATGAG	720		
OY	1101	AAGATGCAACGAGAACTGTGATGTCCTCTGGGGCGTATCTCGACACAGGGGCTGTAC	1160		
DB	721	AAGATGCAACGAGAACTGTGATGTCCTCTGGGGCGTATCTCGACACAGGGGCTGTAC	780		
OY	1161	ATTGTTCATGAGACAGTGTAGCAACCTGTGTGAATTTTCTGCGGAGCCCGGGGTGGA	1220		
DB	781	ATTGTTCATGAGACAGTGTAGCAACCTGTGTGAATTTTCTGCGGAGCCCGGGGTGGA	840		
OY	1221	GCCTCTGTAACACCGCTCAGCTCTCTGAGTTTCTCTGCAAGTGGCCGAGGGCATGGAG	1280		
DB	841	GCCTCTGTAACACCGCTCAGCTCTCTGAGTTTCTCTGCAAGTGGCCGAGGGCATGGAG	900		
OY	1281	TACCTGGAGAGCAAGAGCTTGTGACCGGAGCCTGGGCGCGGCAACATCTGTGGTCTCA	1340		
DB	901	TACCTGGAGAGCAAGAGCTTGTGACCGGAGCCTGGGCGCGGCAACATCTGTGGTCTCA	960		

OY	1341	AAGGAACTGTGGCCAGCAAGTCAGGAGACTT79GGCTGGCCAAAGCCGAGCGAAGGGGCTA	1400
Db	961	GAGGAACTGTGGCCCAAGGTCAGGACTT79GGCTGGCCAAAGCCGAGCGAAGGGGCTA	1020
OY	1401	GATCTAAGACCGGGCTGACCCTCAATGTGACGGCGCCGACAGGCTCTCAAAACACGGGAATTTC	1460
Db	1021	GATCTAAGACCGGGCTGACCCTCAATGTGACGGCGCCGACAGGCTCTCAAAACACGGGAATTTC	1080
OY	1461	ACCAGCAAGTCGATGTCTGTGGAGTT77GGGGTGCTGCTCTGGAGAGTCTTCTCATATGGA	1520
Db	1081	ACCAGCAAGTCGATGTCTGTGGAGTT77GGGGTGCTGCTCTGGAGAGTCTTCTCATATGGA	1140
OY	1521	CGGGCTCGCTACCCCTAAATATGCTACTGAAATAGGTGTCGGAGGCGCGTGGAGAAAGGGGTAC	1580
Db	1141	CGGGCTCGCTACCCCTAAATATGCTACTGAAATAGGTGTCGGAGGCGCGTGGAGAAAGGGGTAC	1200
OY	1581	CGCATGTGAACCCCGGAGGGGCTGTCTCAGAGGCCCCCTGTGACACTGTCTCATATGAGCAGCTGTGG	1640
Db	1201	CGCATGTGAACCCCGGAGGGGCTGTCTCAGAGGCCCCCTGTGACACTGTCTCATATGAGCAGCTGTGG	1260
OY	1641	GAGGCAAGACCCCCCGCCGGCCACACCTTCCGCAAACTGGCCGAGAAAGCT9GGCCCCGGAG	1700
Db	1261	GAGGCAAGACCCCCCGCCGGCCACACCTTCCGCAAACTGGCCGAGAAAGCT9GGCCCCGGAG	1320
OY	1701	CTTAGCGAATGCAAGGTGCCCAAGCCTTCGCTCTCAAGGGCAGAGACGGCAGAGGCTCCACTCTG	1760
Db	1321	CTTAGCGAATGCAAGGTGCCCAAGCCTTCGCTCTCAAGGGCAGAGACGGCAGAGGCTCCACTCTG	1380
OY	1761	CCCCGAAGCCAGAGACCC 1778	
Db	1381	CCCCGAAGCCAGAGACCC 1398	

```

RESULT 9
US-09-741-154-1
; Sequence 1, Application US/09741154
; Patent No. 6437110
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen M. et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1001061
; CURRENT APPLICATION NUMBER: US/09/741.154
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Human
US-09-741-154-1

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Query Match	68.8%	Score 1377;	DB 4;	Length 1713;
Best Local Similarity	99.3%	Pred. No. 7.6e-271;		
Matches 1383; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0;

QY	608	CAGCCTATTGCCGCTGCTCCACAGGGAGATGTCGGGCCAGGAGGCTGTCCACGACTGCA	667
Db	297	CAGCAGCCTTTCGTGGTGTCCACAGGGAAATATCTCGGGCCAGGAGGCTGTCCACGACGTGCA	356
QY	668	GCCCTCCGAGGATGGGGCTTCCGTGCTGGGAGAGTCCGCGGCCACCCCGGCGACTACGT	727
Db	337	GCCTCCGAGGATGGGGCTTTCGTGCTGGGAGAGTCCGCGGCCACCCCGGCGACTACGT	416
QY	728	CCGTGTGCTGAGCTTTGGCCGCGAGAGTATCCACTACCGCGCTGTGTCACCCGCGAGCGCA	787
Db	417	CCTGTGCTGAGCTTTGGCCGCGAGAGTATCCACTACCGCGCTGTGTCACCCGCGAGCGCA	476
QY	788	CCTCAACATGATGAGGCGCGTGTCTTCTGCACACCTCATGAGACATGTTGAGCATTTACAG	847
Db	477	CCATCAACATGATGAGGCGCGTGTCTTCTTGCACCTCATGAGACATGTTGAGCATTTACAG	536

QY	848	CAAGGACAAAGGCGCCGTATCTGCAACCAAGCTGTGTAAACCAAAGGGGAAACACGGGACC	907
Db	537	CAAGGACAAAGGCGCCGTATCTGCAACCAAGCTGTGTAAACCAAAGGGGAAACACGGGACC	596
QY	908	GTGCGCGGAGAGAGACGTGGCCACGAGGGGGCTGTGTTTCTGAACCTGTGACGATTTTGACATT	967
Db	597	GTGCGCGGAGAGAGAGCTGGCCACGAGGGGGCTGTGTTTCTGAACCTGTGACGATTTTGACATT	656
QY	968	GGGAGCACAGATCGGAGAGGGAGAGTGTGAGCTGTCTCGAGGGTGAAGTACCTGGGGCA	1027
Db	657	GGGAGCACAGATCGGAGAGGGAGAGTGTGAGCTGTCTCGAGGGTGAAGTACCTGGGGCA	716
QY	1028	AAAGGTGGCCCTGAAGAATATCAAGTGTGATGTACACAGCCAGGCTTCTGTGACGAGAC	1087
Db	717	AAAGGTGGCCCTGAAGAATATCAAGTGTGATGTACACAGCCAGGCTTCTGTGACGAGAC	776
QY	1088	GGCGGCTATGACGAAGATGCACACAGCAACCTGTGGCTGTCTGTGGGCGGTATCTGCA	1147
Db	777	GGCGGCTATGACGAAGATGCACACAGCAACCTGTGGCTGTCTGTGGGCGGTATCTGCA	836
QY	1148	CCAGGGGCTGTACATTTGTATGAGCAACGTGAGCAAGGGCAACCTGTGTAACTTTCTGCG	1207
Db	837	CCAGGGGCTGTACATTTGTATGAGCAACGTGAGCAAGGGCAACCTGTGTAACTTTCTGCG	896
QY	1208	GACCCGGGGGTGAGAGCCCTCTGTGAACACCCGCTCAGCTCTCTGCAAGTTTTCTCTGCACGTGGC	1267
Db	897	GACCCGGGGGTGAGAGCCCTCTGTGAACACCCGCTCAGCTCTCTGCAAGTTTTCTCTGCACGTGGC	956
QY	1268	CGAGGGCTGTGAGTACCTGTGAGACCAAGAACCTTGTGCACGCGCAACCTGTGGCGGCCCA	1327
Db	957	CGAGGGCTGTGAGTACCTGTGAGACCAAGAACCTTGTGCACGCGCAACCTGTGGCGGCCCA	1016
QY	1328	CATCCTGCTGTACAGAGACCTGTGTGGCCAAAGTACGACATTTTGAGCTGTGGCCAAAGCGA	1387
Db	1017	CATCCTGCTGTACAGAGACCTGTGTGGCCAAAGTACGACATTTTGAGCTGTGGCCAAAGCGA	1076
QY	1388	GCGGAGGGGCTACAGCTCAACCGCGCTGCCCTCAAGTGGAGAGCGCGCCCGGAGGCTGTCA	1447
Db	1077	GCGGAGGGGCTACAGCTCAACCGCGCTGCCCTCAAGTGGAGAGCGCGCCCGGAGGCTGTCA	1136
QY	1448	ACACGGGAAGTTCAACACAGCAGTGGATGTCTGAGATTTTGGGGTGTGCTCTGTGGAGGT	1507
Db	1137	ACACGGGAAGTTCAACACAGCAGTGGATGTCTGAGATTTTGGGGTGTGCTCTGTGGAGGT	1196
QY	1508	CTTCTCATATGAGAGGGGCTCCGTACCCCTAAATGTCACTGGAAGAGGTGTGAGGCCGT	1567
Db	1197	CTTCTCATATGAGAGGGGCTCCGTACCCCTAAATGTCACTGGAAGAGGTGTGAGGCCGT	1256
QY	1568	GGAAGAGGGGTATCCGATGGAACCCCGCGAAGGCTGTCCAGGGCCCGGTGACAGTCTCAT	1627
Db	1257	GGAAGAGGGGTATCCGATGGAACCCCGCGAAGGCTGTCCAGGGCCCGGTGACAGTCTCAT	1316
QY	1628	GAGCAGCTGTGGGAGAGAGCCCGCGCGCGGACCACTTCCGCAAACTGTGCCGAGAA	1687
Db	1317	GAGCAGCTGTGTGGAGAGAGAGCCCGCGCGGACCACTTCCGCAAACTGTGCCGAGAA	1376
QY	1688	GCTGGCCCGGAGACTACGCAAGTGCAGGTGCCCAAGCTTCGCTGTGAGGGCAGAACGCCGA	1747
Db	1377	GCTGGCCCGGAGACTACGCAAGTGCAGGTGCCCAAGCTTCGCTGTGAGGGCAGAACGCCGA	1436
QY	1748	CGGCTTCACCTCGCCCGGCAAGCGAGAACCTTGACCCCAACCGGTTGGGGCCCTTGGCCCG	1807
Db	1437	CGGCTTCACCTCGCCCGGCAAGCGAGAACCTTGACCCCAACCGGTTGGGGCCCTTGGCCCG	1496
QY	1808	AGAGGACCGAGAGTGTGAGAGTGCAGGCGGTGGGGGCACTGACACAGGCCCAAGAGAGGTCC	1867
Db	1497	AGAGGACCGAGAGTGTGAGAGTGCAGGCGGTGGGGGCACTGACACAGGCCCAAGAGAGGTCC	1556
QY	1868	AGGCGGGCAAGTCACTCTCTGTGTGTGCCACACAGAGGGCTGTGCCCAAGTAAAGGGGCTGTG	1927
Db	1557	AGGCGGGCAAGTCACTCTCTGTGTGTGCCACACAGAGGGCTGTGCCCAAGTAAAGGGGCTGTG	1616

OY	1928	GGCGCCCGTGCACACCACAAGCTGGAAGATGATGCCCGATAAAGACGGATTCTAA	1987
Dδ	1617	GGCGCCCGTGCACACCACAAGCTGGAAGATGATGCCCGATAAAGACGGATTCTAA	1676
OY	1988	GGACTCTAAAAA	2000
Dδ	1677	GGAAAAAAAAAAAA	1689

RESULT 10  
US-08-604-989A-8  
: Sequence 8, Application US/08604989A

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: GENERAL INFORMATION:
: APPLICANT: Sakano, S.
: TITLE OF INVENTION: NO. 5834208el Tyrosine Kinase
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennile & Edmonds LLP
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/604,989A
: FILING DATE: February 23, 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Charles E. Miller
: REGISTRATION NUMBER: 24,576
: REFERENCE/DOCKET NUMBER: 1920-026
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 738 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGIN: SOURCE:
: ORGANISM: human
: STRAIN: UT-7
:
: IS-08-604-989A-8

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QY	1194	GTGAACCTTTGGGGAGACCCGGGGGTCAGACCCCTCGTGAACACCGGTCAAGCTCCACATTT	1253
Db	241	GTGAACCTTTTGGGGAGACCCGGGGGTCAGACCCCTCGTGAACACCGGTCAAGCTCCACATTT	300
QY	1254	TCTCTGCACAGTGGCGCGAGGGCATTGAGTAACTCTGGAGAGCAAGAACTTTGTGCACCGGAC	1313
Db	301	TCTCTGCACAGTGGCGCGAGGGCATTGAGTAACTCTGGAGAGCAAGAACTTTGTGCACCGGAC	360
QY	1314	CTGGCCCCCGCCCAATCTCGGTCTCAAGAGACCTGGTGGCCCAAGAGTACAGCACTTTGGC	1373
Db	361	CTGGCCCCCGCCCAATCTCGGTCTCAAGAGACCTGGTGGCCCAAGAGTACAGCACTTTGGC	420
QY	1374	CTGGCCAAAGCCGAGCGGAAGGGGCTAGACTCAAGCCGGCTGCCCGTCAAGTGAAGCGCG	1433
Db	421	CTGGCCAAAGCCGAGCGGAAGGGGCTAGACTCAAGCCGGCTGCCCGTCAAGTGAAGCGCG	480
QY	1434	CCCGAGGCTCTCAAAACCGGGAACTTACCAACGACAGTCGATGTCGTGGAGTTTGGGGTG	1493
Db	481	CCCGAGGCTCTCAAAACCGGGAACTTACCAACGACAGTCGATGTCGTGGAGTTTGGGGTG	540
QY	1494	CTGCTCTGGGAGGTCTTCTCATATGAGACGGGCTCCGTACCCATAAATGTCACTGAAGAG	1553
Db	541	CTGCTCTGGGAGGTCTTCTCATATGAGACGGGCTCCGTACCCATAAATGTCACTGAAGAG	600
QY	1554	GTCTCGGAGGCGCTGTGAGAAAGGGTACCAGATGGAACCCCGCAGGGCTGTCCAGGCCCC	1613
Db	601	GTCTCGGAGGCGCTGTGAGAAAGGGTACCAGATGGAACCCCGCAGGGCTGTCCAGGCCCC	660
QY	1614	GTGCACGTCTCATAGACAGCTGTGTGGAGGCAAGCCCGCCCGCCACCTTTCCG	1673
Db	661	GTGCACGTCTCATAGACAGCTGTGTGGAGGCAAGCCCGCCCGCCACCTTTCCG	720
QY	1674	AAACTGGCCGAGAACTTG	1691
Db	721	AAACTGGCCGAGAACTTG	738

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: RESULT 11
: US-09-741-154-3
: Sequence 3, Application US/09741154
: Patent No. 6437110
: GENERAL INFORMATION:
: APPLICANT: BEASLEY, Ellen M. et al
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: CLO01061
: CURRENT APPLICATION NUMBER: US/09/741,154
: CURRENT FILING DATE: 2000-12-21
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 16389
: TYPE: DNA
: ORGANISM: Human
: US-09-741-154-3

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Query Match	22.8%	Score 455	DB 4	Length 16389
Best Local Similarity	100.0%	Pred. No. 1.3e-83		
Matches 455	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1541	GTCACGTAAAGAGGCTGTCGAGAGCCGTGGAGAAAGGGGTACCGCATGTGAACCCCCCGAGGG	1600	
Db	13941	GTCACGTAAAGAGGCTGTCGAGAGCCGTGGAGAAAGGGGTACCGCATGTGAACCCCCCGAGGG	14001	
QY	1601	CTGTCCAGGGCCCGGTGCAGCTCCTCATGAGCAGCTGCTGGGAGGAGCAGGCCCGCCGCG	1660	
Db	14001	CTGTCCAGGGCCCGGTGCAGCTCCTCATGAGCAGCTGCTGGGAGGAGCAGGCCCGCCGCG	14061	
QY	1661	GCCACCCCTTCGCAAACTGCGCCGAGAAAGTGGCCCGGAGACTAGCAGTGCAGGTGCCCC	1720	
Db	14061	GCCACCCCTTCGCAAACTGCGCCGAGAAAGTGGCCCGGAGACTAGCAGTGCAGGTGCCCC	14121	

QY 1721 AGCTCCGCTCTCAGGCGCAGAGCGCCGACGCTCCACCTCGCCCGGAGCCAGAGCCCTG 1780  
| | | | |  
DB 14121 AGCTCCGCTCTCAGGCGCAGAGCGCCGACGCTCCACCTCGCCCGGAGCCAGAGCCCTG 14180  
| | | | |  
QY 1781 ACCCCACCCGGTGGGGCCCTTGGCCCGCAGAGAGCCGAGAGAGTGGAGAGTCCGGCGTGGG 1840  
| | | | |  
DB 14181 ACCCCACCCGGTGGGGCCCTTGGCCCGCAGAGAGCCGAGAGAGTGGAGAGTCCGGCGTGGG 14240  
| | | | |  
QY 1841 GGCACCTGACAGGCGCCAGAGAGGAGTCCAGGCGGGGCAAGTATCCGCTCGTGGTGGCCACAGC 1900  
| | | | |  
DB 14241 GGCACCTGACAGGCGCCAGAGAGGAGTCCAGGCGGGGCAAGTATCCGCTCGTGGTGGCCACAGC 14300  
| | | | |  
QY 1901 AGGGGCTGGGCCACGTAAGGGGGCTCTGGGCGGCCCTGTGAGACCCGACAGACCTGGCAAGGA 1960  
| | | | |  
DB 14301 AGGGGCTGGGCCACGTAAGGGGGCTCTGGGCGGCCCTGTGAGACCCGACAGACCTGGCAAGGA 14360  
| | | | |  
QY 1961 TGATCGCCCGATTAAGAGCGATTTCTAAGACTCTA 1995  
| | | | |  
DB 14361 TGATCGCCCGATTAAGAGCGATTTCTAAGACTCTA 14395  
| | | | |

## RESULT 12

US-08-604-989A-7  
Sequence 7, Application US/08604989A  
Patent No. 5834208  
GENERAL INFORMATION:  
APPLICANT: Sakano, S.  
TITLE OF INVENTION: No. 5834208el Tyrosine kinase  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennile & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/604,989A  
FILING DATE: February 23, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Charles E. Miller  
REGISTRATION NUMBER: 24,576  
REFERENCE/DOCKET NUMBER: 1920-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: human  
STRAIN: UT-7  
US-08-604-989A-7

Query Match 11.2%; Score 225; DB 2; Length 225;  
Best Local Similarity 100.0%; Pred. No. 3e-37;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 TGGTTCACGGGAGATCTCGGGCCAGAGGCTGTCCAGCAGCTGCAGCCTTCCCGAGAGAT 680  
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DB 1 TGGTTCACGGGAGATCTCGGGCCAGAGGCTGTCCAGCAGCTGCAGCCTTCCCGAGAGAT 60  
| | | | |

QY 681 GGGCTGTCTCTGTGCGGGAGTCCGCGCCACCCCGGAGACTAGTCTGTGGTGAGC 740  
| | | | |  
DB 61 GGGCTGTCTCTGTGCGGGAGATCCGCGCCACCCCGGAGACTAGTCTGTGGTGAGC 120  
| | | | |  
QY 741 TTTGGCCGCGAGCTCATCTACCTACCGCGTGTGTCACCGCGGAGCGCCACCTCAATCGAT 800  
| | | | |  
DB 121 TTTGGCCGCGAGCTCATCTACCTACCGCGTGTGTCACCGCGGAGCGCCACCTCAATCGAT 180  
| | | | |  
QY 801 GAGGCGGTCTCTCTGCAACCTCATGACATGAGTGGAGCAATTAC 845  
| | | | |  
DB 181 GAGGCGGTCTCTCTGCAACCTCATGACATGAGTGGAGCAATTAC 225  
| | | | |

## RESULT 13

US-07-820-011A-3  
Sequence 3, Application US/07820011A  
Patent No. 5336615  
GENERAL INFORMATION:  
APPLICANT: Bell, Leonard  
APPLICANT: Madril, Joseph A.  
APPLICANT: Warren, Stephen L.  
APPLICANT: Luthinger, Daniel J.  
TITLE OF INVENTION: Genetically Engineered  
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced  
TITLE OF INVENTION: Migration  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Maurice M. Klee  
STREET: 1951 Burr Street  
CITY: Fairfield  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06430  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb storage  
COMPUTER: IBM PC XT  
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10  
SOFTWARE: Displaywrite 3  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/820,011A  
FILING DATE: 19920106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Klee, Maurice M.  
REGISTRATION NUMBER: 30,399  
REFERENCE/DOCKET NUMBER: LB-101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 255 1400  
TELEFAX: (203) 254 1101  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1611  
TYPE: NUCLEIC ACID  
STRANDEDNESS: Double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapien  
POSITION IN GENOME:  
PUBLICATION INFORMATION:  
AUTHORS: Anderson, Stephen K.  
AUTHORS: Gibbs, Carol P.  
AUTHORS: Tanaka, Akio  
AUTHORS: Kung, Hsing-jien  
AUTHORS: Fujita, Donald J.  
TITLE: Human Cellular src Gene:  
TITLE: Nucleotide Sequence and Derived Amino  
TITLE: Acid Sequence of the Region Coding for  
TITLE: the Carboxy-Terminal Two-Thirds of







Query Match	10.0%;	Score 199.2;	DB 1;	Length 1602;
Best Local Similarity	-55.7%;	Pred. No. 7.2e-32;		
Matches 453; Conservative	0;	Mismatches 343;	Indels 18;	Gaps 3;

Best Local Similarity 55.78; Pred. NO. 7.2e-32;

Matches 453; Conservative 0; Mismatches 343; Indels 18; Gaps 3;

QY	897	CACGGACACAGTGGCGCCGAGAGAGACTGGCCAGGGCCGGCTGTGTTACGTAACTCGAG	956
Db	736	CCCAACGTCCAAAGCCCCACAGACCACAGGACTGCCACAGAACGGCTGGGAATTCCTCCCGGAG	795
QY	957	CATTGACATTTGGGAGCAGACATCGAGAGGGAGAGTTTGGAGCTGCTGTGCAAGG--T	1013
Db	796	TCCCTGGGGCTGAGGTGAAGCTGGCGGACGGGCTGTTGGGAGAGTGTGATGTGGAGACC	855
QY	1014	GAGTAACTGGGGCAAAAGGTGGCCGTAAAGAAATTCAAG---TGTGATGTGACAGCCGAG	1070
Db	856	TGGAAGGGCAACCAACCAAGGTGGCCATTAAGACTCTGGAAGCCCGGCAACATGTCTCCCGGAG	915
QY	1071	GCTTTCTGACAGAGAGCGCCGTCATGACGAAGAATGCAACACGAAACCTGTGCTGCTC	1130
Db	916	GCTTCTCTGACAGAGAGCCCAAGTATATAGAAAGCTCCGGCATGTGAAAGACTGTTCACGTG	975
QY	1131	CTGGGCGTGAATCTGCACACAGGGGCTGTACATTTGTATGTGACACGCTGAGCAAGGGCAAC	1190
Db	976	TACCACTATGGTGTGGAAGAGCCCATCTACATCTGCTACTGAGTACATGAGCAAGGGAGGC	1035
QY	1191	CTGGTGAACTTTCTGGCGGAGCCCGGGGTGCAAGCCCTCGTGAACACCGCTCAGCTCTCGAG	1250
Db	1036	CTCTGTGATTTCTGGAAGGAGAAATGGGCAAGTACTCTGGCGCTGCCACAGCTGTGCTAT	1095
QY	1251	TTTTCTCTGACAGTGGCCGAGAGGAGATGAGTACTCTGAGAGACAAAGACTTTGTACACGC	1310
Db	1096	ATGGCTGCTCAGATTCGATCCGGCATGGGCTATGTGAGAGATGAATCTAGTGCACAGA	1155
QY	1311	GACCTGGCCGCCGCAACATCTGTGTCTCAGAGAGACTGTGTGCCAAGGTACAGCGACTTT	1370
Db	1156	GACCTGGGGCGCGCAACATCTGTGTGGGGGAGAACTGTGTGTCAAAGGTGGCTGCACTTT	1215
QY	1371	GGCCTGGCCAAAGCGGAGCGGAAGGGGCTGAGCTCAAGCCGGC-----TGGCC	1418
Db	1216	GGGCTGGCACGGCTCATGAGAGACACGAGTACACACACGCAAGGTGCCAAGTTCCCC	1275
QY	1419	GTCAAAGTGAACGGCGCCGAGGCGTCTCAAAACACGGGAAGTTTACACAGACAGTCCGATGTC	1478
Db	1276	ATCAAGTGAADAGGCCCCGAGGACGCCCTGTATGGCGGTTTACACATCAAGTGGAGTGTCTC	1335
QY	1479	TGCAAGTTTGGGGTGTCTCTGTGGAGGTTCTTCTCATATGAGAGGGGCTCCGTACCTTAAA	1538
Db	1336	TGGTCTCTGGCATCTCTGTGACTGACGACTGCCACCAAGGGCCCGGTGGCCATACCCAGGG	1395
QY	1539	ATGTCACATGAAAGAGTGTGGGAGCGCGTGGAGAAAGGGGTATCCGATGGAACCCCGGAG	1598
Db	1396	ATGTTCAACAGGGAGAGTGTCTGTGACACAGGTGAGAGGGGGCTTACCCATGTCCCTGCGCCGC	1455
QY	1599	GCGTGTCCAGGCCCGTGTGACAGTTCATGACAGCACTGTGGAGAGGACAGCCCGCCGC	1658
Db	1456	GAGTGGCCCGAAGTGTGATGCACTCATGTGCAAGGCTGGCGGAGGAGACCCGTGAGAG	1515
QY	1659	CGGCGACCCTTCCGCAAACTGGCGGAAGACTG	1692
Db	1516	CGGCGCACTTTTGATGCTGCAAGGCCCTTCCCTGG	1549

Search completed: September 13, 2003, 02:44:47  
Job time : 147 secs

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GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 13, 2003, 02:41:26 ; Search time 99 Seconds  
(without alignments)  
2260.417 Million cell updates/sec

Title: US-09-977-260-2  
Perfect score: 2671  
Sequence: 1 MAGRSLVSMRAFHCDSAE.....PASVSGQDADGSTRPSRQEP 507

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 segs, 220691566 residues  
Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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-O=/cgn2\_1/USPTO.spool\_p/US09977260/runat\_11092003.141236.18221/app.query.fasta.1.647  
-DB=Issued\_patents\_NA -OFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cd1  
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=p2n -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USPR=US09977260.cgcg\_1.1.85.tunat\_11092003.141236.18221 -NCP=6 -ICP=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -MAIN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

## Database :

Issued Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2671	100.0	1942	2	US-08-604-989A-11
2	2671	100.0	2000	4	US-08-426-509A-1
3	2671	100.0	2000	4	US-08-232-545-1
4	2671	100.0	2000	5	PCT-US95-05008-1
5	2662	99.7	1521	2	US-08-604-989A-10
6	2591.5	97.0	1987	2	US-08-876-882-1
7	2591.5	97.0	1987	4	US-09-315-928-1
8	2444	91.5	1398	2	US-08-604-989A-9
9	2020.5	75.6	1713	4	US-09-741-154-1
10	1469.5	55.0	16389	4	US-09-741-154-3
11	1269	47.5	738	2	US-08-604-989A-8
12	737.5	27.6	1602	1	US-07-820-011A-1

13	737.5	27.6	1602	5	PCT-US93-00445-1	Sequence 1, Appl
14	727	27.2	1611	1	US-07-820-011A-3	Sequence 3, Appl
15	727	27.2	1611	5	PCT-US93-00445-3	Sequence 3, Appl
16	727	27.2	2129	4	US-09-016-434-1452	Sequence 1452, Ap
17	710	26.6	4517	5	PCT-US93-06251-83	Sequence 83, Appl
18	702.5	26.3	2647	4	US-09-220-132-77	Sequence 77, Appl
19	702.5	26.3	2647	5	PCT-US93-06251-77	Sequence 77, Appl
20	691.5	25.9	1491	2	US-09-006-675-1	Sequence 1, Appl
21	691.5	25.9	1491	3	US-09-228-603A-1	Sequence 1, Appl
22	683.5	25.6	3623	1	US-08-306-691B-35	Sequence 35, Appl
23	680	25.5	1467	4	US-09-579-182-2	Sequence 2, Appl
24	680	25.5	1548	4	US-09-099-053-1	Sequence 1, Appl
25	656	24.6	2827	4	US-08-492-723-1	Sequence 1, Appl
26	654.5	24.5	2770	4	US-08-426-509A-5	Sequence 5, Appl
27	654.5	24.5	2770	4	US-08-232-545-5	Sequence 5, Appl
28	654.5	24.5	2770	5	PCT-US95-05008-5	Sequence 5, Appl
C	654.5	24.5	7607	1	US-08-222-616-19	Sequence 19, Appl
C	654.5	24.5	7607	4	US-08-446-648-19	Sequence 19, Appl
C	654.5	24.5	7607	4	PCT-US95-04228-19	Sequence 19, Appl
32	608.5	22.8	2674	4	US-09-817-180-1	Sequence 1, Appl
33	607	22.7	2505	1	US-08-391-615-1	Sequence 1, Appl
34	595.5	22.3	3503	1	US-07-631-717A-1	Sequence 1, Appl
35	595.5	22.3	3503	1	US-08-166-717D-1	Sequence 1, Appl
36	591	22.1	1875	1	US-08-070-165F-3	Sequence 3, Appl
37	591	22.1	1875	2	US-08-885-418-3	Sequence 3, Appl
38	587	22.0	2456	4	US-09-016-434-1476	Sequence 1476, Ap
39	587	22.0	2500	4	US-08-426-509A-3	Sequence 3, Appl
40	587	22.0	2500	4	US-08-232-545-3	Sequence 3, Appl
41	587	22.0	2500	5	PCT-US95-05008-3	Sequence 3, Appl
42	582	21.8	2049	4	US-09-099-749-10	Sequence 10, Appl
43	581.5	21.8	5993	3	US-09-383-630-1	Sequence 1, Appl
44	581.5	21.8	5993	3	US-09-383-630-2	Sequence 2, Appl
45	576.5	21.6	2469	1	US-07-997-133-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-604-989A-11  
Sequence 11 Application US/08604989A  
Patent No. 5834208  
GENERAL INFORMATION:  
APPLICANT: Sakano, S. \*  
TITLE OF INVENTION: No. 5834208el Tyrosine Kinase  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pennile & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/604,989A  
FILING DATE: February 23, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Charles E. Miller  
REGISTRATION NUMBER: 24,576  
REFERENCE/DOCKET NUMBER: 1920-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1942 base pairs  
type: nucleic acid

```

;
; STRANDEDNESS: double
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA to mRNA
;
; ORIGINAL SOURCE:
;
; ORGANISM: human
;
; STRAIN: UT-7
;
; US-08-604-989A-11

Alignment Scores:
Pred. No.: 2,176-257 Length: 1942
Score: 2671.00 Matches: 507
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-977-260-2 (1-507) x US-08-604-989A-11 (1-1942)

QY 1 MetAlaGlyArgGlySerLeuValSerTrpArgAlaPheHisGlyCysAspSerAlaGlu 20
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QY 21 GluLeuProArgValSerProArgPheLeuArgAlaTrpHisProProValSerAla 40
DB GAACCTTCCCGGGTGAAGCCCGGCTTCTCCGAGCCTGGACCCCGCTCCCTCTCAGCC 327
QY 41 ArgMetProThrArgArgTrpAlaProGlyThrGlnCysIleThrLysCysGluHisThr 60
DB AGAGATGCCAAGAGGCGCTGGGGCCCGGGGACCCAGTGTATCACAATGCGAGCACACC 387
QY 61 ArgProLysProGlyGluLeuAlaPheArgLysGlyAspValValThrIleLeuGluAla 80
DB CGCCCAAGGCGAGGAGCTGGCTCCGCAAGGGCGAGCTGTACACATCCTGGAGGCC 447
QY 81 CysGluAsnLysSerTrpTrpArgValLysHisIleThrSerGlyGlnGluLeuLeu 100
DB TGGGAGAACAGAGAGCTGTACCGGCTCAAGCACACACAGTGGAGAGGGGCTGCTG 507
QY 101 AlaAlaGlyAlaLeuArgGluArgGluAlaLeuSerAlaAspProLysLeuSerLeuMet 120
DB GCAGCTGGGGCGCTGGGAGCGGGAGCCCTCCGCAAGACCCCAAGCTCAGCTCATG 567
QY 121 ProTrpPheHisGlyLysIleSerGlyGlnGluAlaValGlnGlnLeuGlnProProGlu 140
DB CCGTGTGTCCAGGGAATCTCGGGCCAGGAGGCTGTCCAGCACCTCGACGCTCCGAG 627
QY 141 AspGlyLeuPheLeuValArgGluSerAlaArgHisProGlyAspTyrValLeuGlyVal 160
DB GATGGGCTGTCTCTGTGGGAGTCCGCGCCGCCACCCCGGCGACTAGCTCTGTGCTG 687
QY 161 SerPheGlyArgAspValIleHisTyrArgValLeuHisArgAspGlyHisLeuThrIle 180
DB AGCTTTGGCGCGGAGCTATCCACTACCGCGTGTGCACCGGAGCGGCACCTCATCATC 747
QY 181 AspGluAlaValPhePheCysAsnLeuMetAspMetValGlnHisTyrSerLysAspLys 200
DB GATGAGGCGCGTGTCTTCTGCAACCTCATGACATGGAGCTGACATTAAGCAAGAGAG 807
QY 201 GlyAlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGlu 220
DB GGGCTATCTGCACCAACCTGTGTGAGACCAAAAGCGAAACAGGAGCAAGTGGCCGAG 867
QY 221 GluGluLeuAlaArgAlaGlyTrpLeuLeuAsnLeuGlnHisLeuThrLeuGlyAlaGln 240
DB GAGGAGCTGGCCAGCGGCGGCTGTACTGAACCTGCAGCATTTGACATTTGGAGCACAG 927
QY 241 IleGlyGluGlyGluPheGlyAlaValLeuGlnGlyGlyTyrLeuGlyGlnLysValAla 260
DB ATCGGAGAGGAGAGAGCTTTGGAGCTGTCTCTGCAAGGTTGAGTACCTTGGCAAAAGGTG 987
QY 261 ValLysAsnIleLysCysAspValThrAlaGlnAlaPheLeuAspGlyThrAlaValMet 280
DB GTGAAGAAATATCAAGTGTGATGTGACAGCCCAAGGCTTCTGTGACGAGAGCGGCTCAT 1047

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QY 281 ThrLysMetGlnHisGluAsnLeuValArgLeuLeuGlyValIleLeuHisGlnGlyLeu 300
DB ACGAAGATGCAACACAGAGAACTGTGGCTCTCTGGGCTGTATCTGTGACACGAGGGCTG 1107
QY 301 TyrIleValMetGlnHisValSerLysGlyAsnLeuValAspPheLeuArgThrArgGly 320
DB TACATTGTATGACACAGTGTGACAAAGGAGCAACTGTGTAACTTCTGTGGAGCCGGGGT 1167
QY 321 ArgAlaLeuValAsnThrAlaGlnLeuLeuGlnPheSerLeuHisValAlaGluGlyMet 340
DB CGAGCGCTGTGTAACACCGCTCAGCTCTCGAGATTTCCTGTACAGTGTGGCCGAGGCAATG 1227
QY 341 GluTyrLeuGluSerLysLysLeuValHisArgAspLeuAlaAlaArgAsnIleLeuVal 360
DB GAGTACTGTGAGAGCAAGAACTTGTGCACCCGAGCACTGGCCCGCGCAACATCCCTGGTTC 1287
QY 361 SerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGluArgLysGly 380
DB TCAGAGGACCTGTGTGGCCAAAGGTGACGCACTTTGGCTGTGGCCAAAGCCGAGGAGGGG 1347
QY 381 LeuAspSerSerArgLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLys 400
DB CTAGACTCAAGCGGCGCTGCCCTCAAGTGCAGCGGCGCCGAGGCTCTCAAAACCGGAGAG 1407
QY 401 PheThrSerLysSerAspValTrpSerPheGlyValLeuLeuTrpGluValPheSerTyr 420
DB TTCACACAGCAAGTGTGATGTGTGAGTTTGGGCTGTGCTGTGGAGAGGCTTCTCATAT 1467
QY 421 GlyArgAlaProTyrProLysMetSerLeuLysGlyValSerGluAlaValGluLysGly 440
DB GGAGCGGCTCTGTACCTTAATAATGTCACTGAAAGAGGTGTGAGAGCCGTGGAGAAAGGGG 1527
QY 441 TyrArgMetGluProProGluGluGlyCysProGlyProValHisValLeuMetSerSerCys 460
DB TACCGCATGGAACCCCGGAGGCGTGTCCAGGCGCCCGCTCATGATGACAGCTGC 1587
QY 461 TrpGluAlaGluProAlaArgArgProPheArgLysLeuAlaGluLysLeuAlaArg 480
DB TGGGAGGAGAGACCCCGCGCGCCGACCTTCCGCAAACTGGCGAGAACTGTGGCCCGG 1647
QY 481 GluLeuArgSerAlaGlyValAlaProAlaSerValSerGlyGlnAspAlaAspLysSerThr 500
DB GAGCTACGAGTGTGAGGTGCCCCAGCTCTCCGTTCAAGGAGGAGGAGGAGGAGGAGGAGG 1707
QY 501 SerProArgSerGlnGluPro 507
DB TCGCCCGCAAGCGCAGAGGCC 1728

RESULT 2
US-08-426-509A-1
; Sequence 1, Application US/08426509A
; Patent No. 6326469
;
; GENERAL INFORMATION:
;
; APPLICANT: Ullrich, Axel
;
; APPLICANT: Gishlitzky, Mikhail
;
; APPLICANT: Sures, Irman G.
;
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
;
; TITLE OF INVENTION: TYROSINE KINASES
;
; NUMBER OF SEQUENCES: 21
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Pennie & Edmonds
;
; STREET: 1155 Avenue of the Americas
;
; CITY: New York,
;
; STATE: NY
;
; COUNTRY: USA
;
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Diskette
;
; COMPUTER: IBM Compatible
;
; OPERATING SYSTEM: DOS
;
; SOFTWARE: FASTSEQ Version 2.0
;
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/426,509A  
FILING DATE: 21-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/232,545  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-0074-999  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2000 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
US-08-426-509A-1

Alignment Scores:  
Pred. No.: 2.27e-257 Length: 2000  
Score: 2671.00 Matches: 507  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-977-260-2 (1-507) x US-08-426-509A-1 (1-2000)

QY 1 Metalaglyarvglyserleuvalsertrparqalapheshisglycysaspseralaglu 20  
DB 258 ATGGCGGGGGAGAGCTTCTGTTTCTGGGGGCAATTCAAGGCTGTGATCTGGTAG 317  
QY 21 GluleuProarValSerProArqPheleuArqalatrPhisProproProValSera 40  
DB 318 GAACCTCCCGGGGAGAGCTTCTGTTTCTGGGGGCAATTCAAGGCTGTGATCTGGTAG 377  
QY 41 ArgMetProthrArqatgtrpAlaproglyThrIncysilethrLysGluHisThr 60  
DB 378 AGGATGCCAAGAGAGCTTGGGCGCGGCAAGGCTGTGATCAACCAATGGAGACACC 437  
QY 61 ArgProLysProgluLysleuAlapharqLysglAspValThrIleuGluAla 80  
DB 438 CGCCCAAGCGAGGGAGCTGCTTCCGCAAGGGGCAAGTGTACCATCTGGAGGCC 497  
QY 81 CysGluAsnLysSerTrpTyrArgValLysHisThrSerGlyGlnGlyLeu 100  
DB 498 TGGGAGAAACAAGACTGTGACCGGCTGCAAGACCAACCAAGTGAAGAGGGCTGCTG 557  
QY 101 AlAlaAlaLysleuAlaArgGluAlaLeuSerAlaAspProLysLeuSerLeuMet 120  
DB 558 GCAAGCTGGGCGCGCGGAGCGGAGGAGGCTTCTCCAGACCCCAAGCTCAGCTCATG 617  
QY 121 ProTrpPheHisGlyLysIleSerGlyGlnGluAlaValGlnGlnLeuGlnProProglu 140  
DB 618 CCGGGGTCCAGGGGAAAGATCTCGGGCCAGAGGCTGTCCAGCAAGCTCAGCTCCGAG 677  
QY 141 AspLysLeuPheLeuValArgGluSerAlaArgHisProgluAspTyrValLeuCysVal 160  
DB 678 GATGGGCTGTCTCGTGGGAGAGTCCGGCGGCCACCCGGCGACTGCTGTGGGTG 737  
QY 161 SerPheGlyArgAspValIleHisTyrArgValLeuHisArgAspGlyHisLeuThrIle 180  
DB 738 AGCTTTGGCGCGCGATCATCACTACCGGCTGTGACCGCGAGCCAGCTCATCATC 797  
QY 181 AspGluAlaValPhePheCysAsnLeuMetAspMetValGluHisTyrSerLysAspLys 200  
DB 798 GATGAGGCGCGTGTCTTCTGCAACCTCATGAGCATGTGTGAGCATTTACAGCAAGGAAAG 857  
QY 201 GlyAlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGlu 220

DB 858 GGGCGATCTGCACCAAGCTGTGTGAGACCAAAAGGGAACAGGAGCAAGTCCGGCAG 917  
QY 221 GluLysLeuAlaArgAlaGlyTTPLeuLeuAsnLeuGlnHisLeuThrLeuGlyAlaGln 240  
DB 918 GAGAGCTGGCGAGGGGGGCTGTACTCAACCTGCAGCATTTGACATTTGGGAGCAG 977  
QY 241 IleGlyGluGlyGluPheGlyAlaValLeuGlnGlyGlyThrLeuGlyGlnValAla 260  
DB 978 ATCGAGAGAGGAGAGTGTGGAGCTGTCTGCAAGGCTAGTACTGGGGCAAAAGTGGCC 1037  
QY 261 ValLysAsnLysCysAspValThrAlaGlnAlaPheLeuAspGluThrAlaValMet 280  
DB 1038 GTGAAGAATATCAAGTGTGATGTGACAGCCAGGCTTCTCGAGCAGAGAGCGCGCATG 1097  
QY 281 ThrLysMetGlnHisGluAsnLeuValArgLeuGlnGlyAlaIleLeuHisGlnGlyLeu 300  
DB 1098 ACGAAGATGCACACGAGAACCTGTGCTCTGTGGCGGTGATCTGCACACAGGGGCTG 1157  
QY 301 TyrIleValMetGluHisValSerLysGlyAsnLeuValAsnPheLeuArgThrArgGly 320  
DB 1158 TACATTTCTATGAGCACGAGAGAGGCAACCTGTGATCTTCTGGGAGCCGGGCT 1217  
QY 321 ArgAlaLeuValAsnThrAlaGlnLeuGlnPheSerLeuHisValAlaGluGlyMet 340  
DB 1218 CGAGCCCTCGTAACACCGGCTCAGCTCTGAGATTTCTCTGCAAGCGGCGAGGCGCATG 1277  
QY 341 GluTyrLeuGlnSerLysLysLeuValHisArgAspLeuAlaAlaArgAsnIleLeuVal 360  
DB 1278 GAGTACCTGTGAGACCAAGAGCTGTGTACCGGCAAGCTGTGGCGCCCAACATCTGTGTC 1337  
QY 361 SerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGluArgLysGly 380  
DB 1338 TCAGAGACCTGTGGGCGCAAGTGTAGCGACTTTGGCTGTGGCCAAAGCCGAGCGAAGGG 1397  
QY 381 LeuAspSerSerArgLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLys 400  
DB 1398 CTAGACTCAAGCCGGCTGCGCGTCAAGTGAAGGAGCGCGCGGCTGTCAAAACAGCGAAG 1457  
QY 401 PheThrSerLysSerAspValTTPSerPheGlyAlaLeuLeuTrpGluValPheSerTyr 420  
DB 1458 TTCACCAAGAGTGGATGTGTGGATTTGGGGGTGTCTGTGGAGGTTCTTCATAT 1517  
QY 421 GlyArgAlaProTyrProLysMetSerLeuLysGluValSerGluAlaValGluLysGly 440  
DB 1518 GGAGGGGCTCGTACCTTAATGTCACTGAAGAAGTGTGGAGGCGGTGGAGAAGGGC 1577  
QY 441 TyrArgMetGluProProgluGlyCysProgluProValHisValLeuMetSerSerCys 460  
DB 1578 TACCGATGGAACCCCGGAGGGCTGTGCAAGGCCCGGTGCACGTCTCATGAGCAGCTGC 1637  
QY 461 TrpGluAlaGluProAlaAlaArgArgProProPheArgLysLeuAlaGluLysLeuAlaArg 480  
DB 1638 TGGGAGGACAGCCCGCGCGGCGGCAAGCTTCCGCAAACTGGCGGAGAACTGGCCGG 1697  
QY 481 GluLeuArgSerAlaGlyAlaProAlaSerValSerGlyGlnAspAlaAspGlySerThr 500  
DB 1698 GAGCTAGCAGATGAGAGGTGCCCAAGCTCGTCTCAGGGCAGAGACCGGAGGCTCCACC 1757  
QY 501 SerProArgSerGlnGluPro 507  
DB 1758 TCGGCCCGAAGCCAGAGGCC 1778

RESULT 3  
US-08-232-545-1  
Sequence 1, Application US/08232545  
Patent No. 6506578  
GENERAL INFORMATION:  
APPLICANT: Glitsky, Axel  
APPLICANT: Glitsky, Mikhail  
APPLICANT: Sures, Irmay G.  
TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine  
TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/232,545  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)790-9090  
TELEFAX: (212)869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2000 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA  
US-08-232-545-1  
Alignment Scores:  
Pred. No.: 2, 27e-257 Length: 2000  
Score: 2671.00 Matches: 507  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-977-260-2 (1-507) x US-08-232-545-1 (1-2000)  
QY 1 MetAlaGlyArgGlySerLeuValSerTrpArgAlaPheHisGlyCysAspSerAlaGlu 20  
DB 258 ATGGGGGGGGGAGGCTCTGCTGTTCTGCGGCGCATTCACGGCTGATTCGCTGAG 317  
QY 21 GluLeuProArgValSerProArgPheLeuArgAlaTrpHisProProValSerAla 40  
DB 318 GAACCTTCCCCGGGTGAGCCCCGCTTCCTCCGAGCCTGGACCCCCCTCCGCTCAGCC 377  
QY 41 ArgMetProThrArgArgTrpAlaProGlyThrGlnCysIleThrLysCysGlnHisThr 60  
DB 378 AGGATGCCAAGAGGGCGCTGGGCCCCGGGCGACCAAGTGTATGACCAAAAGCAGCAGACC 437  
QY 61 ArgProLysProGlyGluLeuAlaPheArgLysGlyAspValValThrIleLeuGluAla 80  
DB 438 CCCCCCAAGCCAGGGGAGCTGGCTTCGCGAAGGGCGAGCTGTGATCCATCTCGAGGCC 497  
QY 81 CysGluAsnLysSerTrpTrpArgValLysHisHisThrSerGlyGlnGluLeuLeu 100  
DB 498 TCGGAGAACAGAGCTGGTACCGGCTCAAGCAGCACACAGACAGAGAGGGGCTGTG 557  
QY 101 AlaAlaGlyAlaLeuArgGluArgGluAlaLeuSerAlaAspProLysLeuSerLeuMet 120  
DB 558 GCAGCTGGGGCCCTCGGGAGGCGGAGGAGCCCTTCGCGAGACCCCAAGCTCAGCTCATG 617  
QY 121 ProTrpPheHisGlyLysIleSerGlyGlnGluAlaValGlnGlnLeuGlnProProGlu 140  
DB 618 CCGTGGTTCACAGGAGATCTCGGGCGAGGAGCTGTGCACAGCTGAGCCTCCGCGAG 677  
QY 141 AspGlyLeuPheLeuValArgGluSerAlaArgHisProGlyAspTyrValLeuCysVal 160

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DB 678 GATGGGCTGTCTCGTGGGGAGTCCGGGCGCACCCGGGACATACCTCTGTCGGG 737  
QY 161 SerPheGlyArgAspValIleHisTrpArgValLeuHisArgAspGlyHisLeuThrIle 180  
DB 738 AGCTTTGGCGCGAGCTCATCCACTCCCGCTCTGACCGGAGGCCACCTCACAAATC 797  
QY 181 AspGluAlaValPhePheCysAsnLeuMetAspMetValGluHisTyrSerLysAspLys 200  
DB 798 GATGAGCGCGTGTCTTCTGCAACCTCATGAGCATGTGGAGCATTAAGCAAGCAAG 857  
QY 201 GlyAlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGlu 220  
DB 858 GGGCTATGTGACCAAGCTGGTGAACCAAGCGGAAACGGGACCAAGTGGCGGAG 917  
QY 221 GluGluLeuAlaArgAlaGlyTrpLeuLeuAsnLeuGlnHisLeuThrLeuGlyAlaGln 240  
DB 918 GAGGAGCTGGCCAGGGCGGGGCTGTGATTACGAACTCTGACATTTGACATTGGAGGACAG 977  
QY 241 IleGlyGluGlyGluPheGlyAlaValLeuGlnGlyGluTyrLeuGlyGlnLysValAla 260  
DB 978 ATCGCAGAGGAGAGTTTGAGCTCTGCGAGGGTGAATACCTGGGCGCAAAAGTGGCC 1037  
QY 261 ValLysAsnIleLysCysAspValIleThrAlaGlnAlaPheLeuAspGlyThrAlaValMet 280  
DB 1038 GTGAAGAAATATCAAGTGTATGTGACAGCCAGGCTTCTGAGCAGAGCGCTTCATG 1097  
QY 281 ThrLysMetGlnHisGluAsnLeuValArgLeuGlyValIleLeuHisGlnGlyLeu 300  
DB 1098 ACGAAGATGCACACAGCAAGAACTGTGGCTCTCTGGGGGTATCTTGACACAGGGGCTG 1157  
QY 301 TyrIleValMetGluHisValSerLysGlyAsnLeuValAsnPheLeuArgThrArgGly 320  
DB 1158 TACATGTGATGAGAGACGTGAGCAAGGGCAACTGTGAACTTCTCGGAGCCCGGGGT 1217  
QY 321 ArgAlaLeuValAsnThrAlaGlnLeuGlnPheSerLeuHisValAlaGluGlyMet 340  
DB 1218 CGAGCCCTGTGAACACCGCTCAGCTCTGCAAGTTTCTCTCAGCTGGCCAGGGCAGG 1277  
QY 341 GluTyrLeuGluSerLysLysLeuValHisArgAspLeuAlaAlaArgAsnIleLeuVal 360  
DB 1278 GAGTACCTGGAGAGCAAGAGCTTGTGCAACCCGAGACTGGCCCGCGCAACATCTCGTGC 1337  
QY 361 SerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGluArgLysGly 380  
DB 1338 TCAGAGGAGACTGTGTGGCCAAAGTCCAGGCACTTGGCTTGCCAAAGCCGAGAGGGG 1397  
QY 381 LeuAspSerSerArgLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLys 400  
DB 1398 CTGAGCTCAAGCCGGCTGCCCTCAAGTGGAGCGGCCGGAAGCTTCAAAACGGGAGG 1457  
QY 401 PheThrSerLysSerAspValIlePhePheGlyValLeuLeuTrpGluValPheSerTyr 420  
DB 1458 TTCACACAGCAAGTCGAGATGTCTGAGATTGTGGGGTGTCTCTGGGAGGTCTTCATAT 1517  
QY 421 GlyArgAlaProTyrProLysMetSerLeuLysGluValSerGluAlaValGluLysGly 440  
DB 1518 GGACGGGCTCCCTACCTAAATATGCACGAAAGAGGTGTCCGAGAGCCGTGAGAGAGGGG 1577  
QY 441 TyrArgMetGluProProGluGlyCysProGlyProValHisValLeuMetSerCys 460  
DB 1578 TACCGCATGGAAACCCCGGAGGGCTGTCCAGGCCCGCTGACGTCTCTTGAGCAAGTGC 1637  
QY 461 TrpGluAlaGluProAlaArgArgProPheArgLysLeuAlaGluLysLeuAlaArg 480  
DB 1638 TGGAGAGCAGAGACCCGCGCGGCGACCTTCGCCAAATGCGCGAAGAGCTGGCCGG 1697  
QY 481 GluLeuArgSerAlaGlyAlaProAlaSerValSerGlyGlnAspAlaAspGlySerThr 500  
DB 1698 GAGCTAACGAGTGCAGAGTGGCCCAAGCTCCGTTGACGAGGACAGGAGCGGCTCCACC 1757  
QY 501 SerProArgSerGlnGluPro 507  
|||||

Db 1758 TCGCCCCGAGCCAGAGCCC 1778

RESULT 4  
PCT-US95-05008-1  
Sequence 1, Application PC/TUS9505008  
GENERAL INFORMATION:  
APPLICANT: Sugen, Inc.  
APPLICANT: 515 Galveston Drive  
APPLICANT: Redwood City, California 94063-4720  
APPLICANT: United States of America  
APPLICANT: Wissenschaften E.V.  
APPLICANT: München 80539  
APPLICANT: Germany  
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05008  
FILING DATE: 24-APR-1995  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/232,545  
FILING DATE: 22-APR-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cornuzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-074  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)790-9090  
TELEFAX: (212)869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2000 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA  
PCT-US95-05008-1

Alignment Scores:  
Pred. No.: 2,27e-257 Length: 2000  
Score: 2671.00 Matches: 507  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-09-977-260-2 (1-507) x PCT-US95-05008-1 (1-2000)

QY 1 MetalGlyArgGlySerLeuValSerTPARAlaPheHisIcysAspSerAlaGlu 20  
Db 258 ATGGCGGGGAGAGCTCTCTGCTTCCTGGCGGGCATTCACGCGTGTGATTCGTGAG 317  
QY 21 GluLeuProArgValSerProArgPheLeuValArgAlaThrHisProProValSerAla 40  
Db 318 GAACCTCCCGGGGTGAGCCCCCGCTTCCTCGAGCGTGGACACCCCTCCCGTCTCAGCC 377  
QY 41 ArgMetProThrArgTrpAlaProGlyThrGlnCysIleThrIlyscysGluHisThr 60

Db 378 AGGATGCGACAGAGCGCGCTGGCCCGCGGACACCAAGTATACCAAAATCGAGACACACC 437  
QY 61 ArgProIlySerProGlyGluLeuAlaPheArgIlycysPValThrIleGluAla 80  
Db 438 CGCCCCAAGCCAGAGGGGAGCGGCTTCGCCAAGGGGACCTGGTACACATCCCTGGAGGCC 497  
QY 81 CysGluAsnIlySerTPYrArgValIlyHisIsthSerGlyGlnIlyGluLeu 100  
Db 498 TCGGAGACAGAGCTGTGACCGCGTCAACACACACAGTGAGACAGGAGGGCTGTG 557  
QY 101 AlaAlaGlyAlaLeuArgGluArgGluAlaLeuSerAlaAspProIlySerLeuMet 120  
Db 558 GCAGCTGGGGCGGTGGGGGAGCGGAGGCCCTCTCCGACACCCCAAGCTCAGCTCATG 617  
QY 121 ProTrpPheHisGlyIlySerGlyGlnAlaValIlnGlnLeuGlnProProGlu 140  
Db 618 CCGTGTTCACCGGGAAGATCTCGGGCAGAGGCTTCCAGCAGCTGCAGCCCTCCGAG 677  
QY 141 AspGlyLeuPheLeuValArgGluSerAlaArgHisProGlyAspTrpValLeuCysVal 160  
Db 678 GATGGCTGTTCCTGTGGGGAGTCCGGCCGACCCCGGCHTACGTCTGTGCTG 737  
QY 161 SerPheGlyArgAspValIleHisIlyrArgValLeuHisArgAspGlyHisIleuThrIle 180  
Db 738 AGCTTGGCGCGGCGCATCCATCCAGCTGCTGACCGCGGACCGGCGCACCATCATC 797  
QY 181 AspGluAlaValPhePheCysAsnLeuMetAspMetValIlnIlyrSerIlyAspIly 200  
Db 798 GATGAGCGCGCTGTCTCTCCACCTCATGAGATGGTGGAGCTTTCACACAGGACACAG 857  
QY 201 GlyAlaIleCysThrIlycysAspValArgProIlyArgIlyHisGlyThrIlySerAlaGlu 220  
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QY 918 GAGGAGCTGGCCAGCGCGGCGCTGTCTGACCTGCAGCATTTGACATTTGGGAGCACAG 977  
QY 241 IleGlyGluGlyIlyPheGlyAlaValLeuGlnGlyIlyrIleuGlyIlycysValAla 260  
Db 978 ATCGGAGAGGAGATTTGGAGCTGTCTCAGAGGTGAGTACCTGGGGGCAAAAGTGGCC 1037  
QY 261 ValIlyAsnIleIlycysAspValThrAlaGlnAlaPheLeuAspGlyThrAlaValMet 280  
Db 1038 GTGAGAGATATCAAGTGTGATGTGACAGCCAGGCTTCTCGGACGAGAGCGCGTATG 1097  
QY 281 ThrIlyMetGlnHisGluAsnLeuValArgLeuLeuGlyAlaIleLeuHisGlnIlyLeu 300  
Db 1098 ACGAAGATGCACACAGCAAGACGTGTGCTCTCTGGCGGTGATCTGCACACAGGGCTG 1157  
QY 301 TyrIleValMetGluHisValSerIlycysGlyAsnLeuValAsnPheLeuArgThrArgGly 320  
Db 1158 TACATGTGCATGGAGCAGCTGTGACCAAGGGCAACCTGTGTGAACCTTTCGCGACCCGGGGT 1217  
QY 321 ArgAlaLeuValAsnThrAlaGlnIleuGlnIlyPheSerLeuHisValAlaGluGlyMet 340  
Db 1218 CGAGCCCTGTGAACACCGCTCAGCTCTCAGATTTCTTGACGCGGGGAGGGCATG 1277  
QY 341 GluTrpLeuGluSerIlycysLeuValHisArgAspLeuAlaIlaArgAsnIleLeuVal 360  
Db 1278 GAGTACCTGGAGAGCAAGAAAGCTGTGTGCACGGGAGCTGGCCGCGCAACATCTGTGTC 1337  
QY 361 SerGluAspLeuValAlaIlycysValSerAspPheGlyLeuAlaIlycysAlaGluArgGly 380  
Db 1338 TCAGAGAGACCTGTGTGGCAAGAGTCAAGCATTTGTGCTTGCACCAAGCGGAGGGG 1397  
QY 381 LeuAspSerSerArgLeuProValIlyrTrpThrAlaProGluAlaLeuHisGlyIly 400  
Db 1398 CTGAGCTCAAGCGCGCTGCGCTCAAGTGGACGGCGGCGGAGCTTCAACACAGGGAG 1457  
QY 401 PheThrSerIlySerAspValTrpSerPheGlyValLeuLeuTrpGluValPheSerTyr 420





Db 1021 GAGTACTGGAGACCAAGACCTTGTGCACCGCAGCCTGGCCGCCGCAACATCTGTGTC 1080  
Qy 361 SerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaArgLysGly 380  
Db 1081 TCAGAGGACCTGGTGGCCAGAGGTCAAGACTTTGGCTGGCCAAAGCCGAGAGGGGG 1140  
Qy 381 LeuAspSerSerArgLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLys 400  
Db 1141 CTAGACTCAAGCCGGCTGCCCCGTCAAGTGAAGGAGGCTGGAGCGCTCTCAAAACAGGGAG 1200  
Qy 401 PheThrSerLysSerAspValTrpSerPheGlyValLeuLeuTrpGluValPheSerTyr 420  
Db 1201 TTCACGACGACAGTGGTGTCTGTGAGATTGGGGTGTGCTGCTGGAGGAGTCTTCTCATAT 1260  
Qy 421 GLYArgAlaProGlyTrpProLysMetSerLeuLysGlyValSerGlyValAlaValGlyLysGly 440  
Db 1261 GGACGGGCTCCGTACCTTAATAATGTCACTGAAGAAGGTGTGGAGCGCTGTGAAGAAGGGG 1320  
Qy 441 TyrArgMetGluProProGluGlyLysProGlyProValHisValLeuMetSerSerCys 460  
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Qy 461 TrpGluAlaGluProAlaAlaArgArgProProPheArgLysLeuAlaGlyLysLeuAlaArg 480  
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Qy 481 GluLeuArgSerArgLysAlaGlyAlaProAlaSerValSerGlyHisAspAlaAspGlySerThr 500  
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Qy 501 SerProArgSerGlnGluPro 507  
Db 1501 TCGCCCGCAAGCCAGAGGCC 1521

RESULT 6  
US-08-876-882-1  
: Sequence 1, Application US/08876882  
: Patent No. 5981201  
: GENERAL INFORMATION:  
: APPLICANT: Avraham, Hava  
: TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT  
: TITLE OF INVENTION: OF BREAST CANCER  
: NUMBER OF SEQUENCES: 9  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds P. C.  
: STREET: Two Militia Drive  
: CITY: Lexington  
: STATE: MA  
: COUNTRY: USA  
: ZIP: 02173-4799  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: Windows  
: SOFTWARE: FastSeq for Windows Version 2.0b  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/876,882  
: FILING DATE: 16-JUN-1997  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 60/035,228  
: FILING DATE: 08-JAN-1997  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Doreen, Hogle M  
: REGISTRATION NUMBER: 36,361  
: REFERENCE/DOCKET NUMBER: MEDH97-01PA  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 781-861-6240  
: TELEFAX: 781-861-9540  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1987 base pairs

: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: CDNA  
US-08-876-882-1  
Alignment Scores:  
Pred. No.: 2,02e-249 Length: 1987  
Score: 2591.50 Matches: 502  
Percent Similarity: 99.21% Conservative: 1  
Best Local Similarity: 99.01% Mismatches: 3  
Query Match: 97.02% Indels: 3  
Gaps: 1  
US-09-977-260-2 (1-507) x US-08-876-882-1 (1-1987)  
Qy 1 MetaLacIyArgGlySerLeuValSerTrpArgAlaPheHisGlyCysAspSerAlaGlu 20  
Db 263 ATGGCGGGGAGAGCTCTCTGTTTCCGTGGCGGCATTTCAAGGCTGTGATTTGTGTAG 322  
Qy 21 GluLeuProArgValSerProArgPheLeuAlaArgAlaTrpHisProProProValSerAla 40  
Db 323 GAACCTCCCGGGGTAGCCCGCTCTCTCCGAGCCTGGACCCCTCCCTCCGCTCAGCC 382  
Qy 41 ArgMetProThrArgArgTrpAlaProGlyThrGlnCysIleThrLysCysGluHisThr 60  
Db 383 AGGATGCCAACAGAGCGCTGGGCCCGGCGACCCAGTGTATACCCAAATGGAGACACACC 442  
Qy 61 ArgProLysProGlyGlyLeuAlaPheArgLysGlyAspValValThrIleLeuGluAla 80  
Db 443 CGCCCAAGCCAGGGAGAGCTGGCTCCGCAAGGGGCGACGTGCACCATCTGTGAGGCC 502  
Qy 81 CysGluAsnLysSerTrpTrpArgValLysHisHisThrSerGlyGlnGlyLeu 100  
Db 503 TGCAGAAACAAGACTGTGTACCGGTCAAGCACACACACATGTGACAGAGGGCTGTG 562  
Qy 101 AlaAlaGlyAlaLeuArgGluArgGluAlaLeuSerAlaAspProLysLeuSerLeuMet 120  
Db 563 GCAGCTGGGGGCGTGGCGGAGGGAGGCCCTTCCGACAGACCCCAAGCTAGGCTCATG 622  
Qy 121 ProTrpPheHisGlyLysIleSerGlyGlnGluAlaValGlnGlnLeuGlnProProGlu 140  
Db 623 CCGTGTCCACAGGAGATCTCGGCGAGGAGCTGCCAGACCTGCACGCTCAGCCGAG 682  
Qy 141 AspGlyLeuPheLeuValArgGluSerAlaArgHisProGlyAspTrpValLeuCysVal 160  
Db 683 GATGGCTGTCTCTGTGGTGGGAGTCCGCGCCACCCCGGCACTACGTCTGTGGCTG 742  
Qy 161 SerPheGlyArgAspValIleHisTyrArgValLeuHisArgAspGlyHisLeuThrIle 180  
Db 743 AGCTTTGGCCCGCAGCTCATCTACCGCTGCTGCACCGCGCACGGCCACTGCATCAATC 802  
Qy 181 AspGluAlaValPhePheCysAsnLeuMetAspMetValGlnHisTyrSerLysAspLys 200  
Db 803 GATGAGGCGCGTCTCTGCAACCTCATGACATGTGGAGCATTTACAGCAAGACAG 862  
Qy 201 GlyAlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGlu 220  
Db 863 GGCCTATCTGCACCAAGCTGTGAGACCAAGCGGAACCGGAGCCAAATGTGGCGAG 922  
Qy 221 GluGluLeuAlaArgAlaGlyTrpLeuLeuAsnLeuGlnHisLysLeuThrLeuGlyValAla 240  
Db 923 GAGAGCTGGCGCAGGGCGGCTGTGTACTGAACCTGCAGCATTTGTGACATTTGGAGCAG 982  
Qy 241 IleGlyGluGlyLysPheGlyAlaValLeuGlnGlyLysLysValAla 260  
Db 983 ATCGAGAGGAGGAGATTGTGAGCTGTCTGCAGGAGTGTACTCTGGGGCAAAAGGTGGCC 1042  
Qy 261 ValLysAsnIleLysCysAspValThrAlaGlnAlaPheLeuAspGlyThrAlaValMet 280  
Db 1043 GTGAAGATATCAAGTGTGATGACAGCCCAAGGCTTCTTCGAGCAAGACCGCGTCAATG 1102  
Qy 281 ThrLysMetGlnHisGluAsnLeuValArgLeuLeuGlyValIleLeuHisGlnGlyLeu 300

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Db 1103 ACGAATATGCACACAGAACCGTGGCTCTCTCTGGGGTGTCTCGACACCGGGGCTG 1162
QY 301 TTTTLeValMetClnHisValSerLysGlyAsnLeuValAsnPhenLeuArgThrArgGly 320
Db 1163 TACATTGTGATGAGACGACGTGAGCAGGCGACACCTGTGACTTTTCTGGCGACCCGGGGT 1222
QY 321 ArgAlaLeuValAsnThrAlaGlnLeuLeuGlnPheSerLeuHisValAlaGlnGlyMet 340
Db 1223 CGAGCCCTGCTGTAACACCGCTCAGCTCTGACATTTTCTCTGACGCTGGCGGAGGCAATG 1282
QY 341 GlnTyrLeuGlnSerLysLysLeuValHisArgAspLeuAlaAlaArgAsnIleLeuVal 360
Db 1283 GAGTACCTGAGAGCAGAGAGCTTGTGCACCGGAGCTGGCCGCCGCAACATCCGCGTGC 1342
QY 361 SerGlnAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGlnArgGlyGly 380
Db 1343 TCGAGGAGCTGTGGCCCAAGGTCACGACTTTGGCCCTGGCCCAAGCCGAGCGGAAGGGG 1402
QY 381 LeuAspSerSerArgLeuProValLysTyrThrAlaProGlnAlaLeuLysHisGlyLys 400
Db 1403 CTGAGCTCAAGCGCGCTGCCCTCAAGTGAGCGCGCCGAGGCTCTCAAAACACGGG --- 1459
QY 401 PheThrSerLysSerAspValTyrSerPheGlyValLeuLeuTrrpGlnValPheSerTyr 420
Db 1460 TTCACACGAGAGTGGATGTGTGAGCTTTGGGGTCTGCTGGGAGAGGCTTCTCATAT 1519
QY 421 GlyArgAlaProTyrProLysMetSerLeuLysGlnValSerGlnAlaValGlnLysGly 440
Db 1520 GAGCGGGCTCCGACCTTAAATGTACAGTGAAGAGCTGTCCGAGGCCGCTGGGAGGAAGGG 1579
QY 441 TyrArgMetGlnProGlnGlyCysProGlyProValHisValLeuMetSerSerCys 460
Db 1580 TACCGCATGGAACCCCGCCGAGGGCTGTCCAGCGCCGCTGCATGAGACAGCTGC 1639
QY 461 TrpGlnAlaGlnProAlaArgArgProPheArgLysLeuAlaGlnLysLeuAlaArg 480
Db 1640 TGGAGGACAGAGCGGCC -CGCGCGCACCCCTCCGAAACTGGCCAGAGAGCTGGCCGG 1698
QY 481 GlnLeuArgSerAlaGlnAlaProAlaSerValSerGlyGlnAspAlaAspGlySerThr 500
Db 1699 GAGCTACGACAGTGCAGAGTCCGCCAGGCTCTGTCAGGAGGAGAGCCGCCAGCGTCC -ACC 1757
QY 501 SerProArgSerGlnGlnPro 507
Db 1758 TCGCCCCGAAAGCCAGAGGCC 1778

RESULT 7
US-09-315-928-1
; Sequence 1, Application US/09315928
; Patent No. 6368796
; GENERAL INFORMATION:
; APPLICANT: Avraham, Hava
; APPLICANT: Croopman, Jerome E.
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; FILE REFERENCE: NEDH97-01PAZ
; CURRENT APPLICATION NUMBER: US/09/315,928
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 08/876,882
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 60/035,228
; PRIOR FILING DATE: 1997-01-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)...(1846)
US-09-315-928-1
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Alignment Scores:
Pred. No.: 2,02e-249 Length: 1987
Score: 2591.50 Matches: 502
Percent Similarity: 99.21% Conservative: 1
Best Local Similarity: 99.01% Mismatches: 3
Query Match: 97.02% Indels: 3
DB: 4 Gaps: 1

US-09-977-260-2 (1-507) x US-09-315-928-1 (1-1987)
QY 1 MetAlaGlyArgGlySerLeuValSerTrrpArgAlaPheHisGlyCysAspSerAlaGln 20
Db 263 ATGCGGGGGAGAGCTCTGTGGTTCTCTGGCGGGCATTTCCACGCGTGTGATTCGTGAG 322
QY 21 GlnLeuProArgValSerProArgPheLeuArgAlaTrrpHisProProProValSerAla 40
Db 323 GAACCTTCCCGGGGTGAGCCCGCCCTTCTCCAGCTGGACCCCTCCGCTCTAGCC 382
QY 41 ArgMetProThrArgArgTrrpAlaProGlyThrGlnCysIleThrLysCysGlnHisThr 60
Db 383 AGGATGCAACGAGAGGGCTGGCCCGCGGACCCAGTGTATCACAATGCGAGCACACC 442
QY 61 ArgProLysProGlyGlnLeuAlaPheArgLysGlyAspValAlaThrIleLeuGlnAla 80
Db 443 CGCCCAAGCCAGGGAGAGCTGGCTCCGCAAGGGGAGACGTGTGTACACATCCGAGGCC 502
QY 81 CysGlnAsnLysSerTrrpTyrArgValLysHisHisThrSerGlyGlnGlnGlyLeu 100
Db 503 TCGCAAGACAGAGCTGTGATCCCGCTCAGACACACACACGATGAGACAGAGGGCTGTG 562
QY 101 AlaAlaGlyAlaLeuArgGlnArgGlnAlaLeuSerAlaAspProLysLeuSerLeuMet 120
Db 563 GCAGCTGGGGCGCTGGGGAGCGGGAGAGGCCCTCTCCGACAGACCCCAAGCTCAGCTCATG 622
QY 121 ProTrrpPheHisGlyLysIleSerGlyGlnGlnAlaValGlnGlnLeuGlnProProGln 140
Db 623 CCTGTGTTCACCGGAGAGCTGTGGCCAGAGAGCTGTCCAGAGCTGCGCTCCCGAG 682
QY 141 AspGlyLeuPheLeuValArgGlnSerAlaArgHisProGlyAspTrrpValLeuCysVal 160
Db 683 GATGGGCTGTCTCTGTGGCGGAGTCCGGCGCCACCCCGCCACATACGCTCTGTGCTG 742
QY 161 SerPheGlyArgAspValIleHisTyrArgValLeuHisArgAspGlyHisLeuThrIle 180
Db 743 AGCTTTGGCCGCGACGTCATCCATCCGCGTGTCCAGCGGACGCGCCACTCACATTC 802
QY 181 AspGlnAlaValAlaPhePheCysAsnLeuMetAspMetValGlnHisTyrSerLysAspLys 200
Db 803 GATGAGCGCGTGTCTTGTGCAACCTCATGTGACATGTGTGAGCATTTACAGACAGGACAG 862
QY 201 GlyAlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGln 220
Db 863 GCGGCTATCTGCCCAAGCTGGTGAGACCAACAGCGAAGACCGGACCAAGTGGCCGAG 922
QY 221 GlnGlnLeuAlaArgAlaGlyTrrpLeuLeuAsnLeuGlnHisLeuThrLeuGlnAlaGln 240
Db 923 GAGGAGCTGGCCAGGGCGGGCGGTGTACTGAACCTGCAGCATTTGACATTTGGAGACAG 982
QY 241 IleGlyGlnGlyGlnPheGlyAlaValLeuGlnGlyGlnTyrTrrpLeuGlnLysValAla 260
Db 983 ATCGGAGAGGAGAGTGTGAGCTGTCTGACAGGTGAGTACCTGGGGCAAAAGTGGGCC 1042
QY 261 ValLysAsnIleLysCysAspValTrrpAlaGlnAlaPheLeuAspGlnTrrpAlaValMet 280
Db 1043 GTGAGAGATTTCAAGTGTGTGACAGCCCAAGCCCTTCTTGACAGACAGCGCCGTATG 1102
QY 281 ThrLysMetGlnHisGlnAsnLeuValArgLeuLeuGlyValIleLeuHisGlnGlyLeu 300
Db 1103 ACGAAGATGCAACAGAGAACTGTGGTCTCTCTGGCGGTGATCTGCACACGAGGGGCTG 1162
QY 301 TTTTLeValMetClnHisValSerLysGlyAsnLeuValAsnPhenLeuArgThrArgGly 320
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Db 1163 TACATTGTGATGGACGACGTGAGCAAGGCAACCTGGTGAACCTTTCGCGAGCCGGGGT 1222  
Qy 321 ArgAlaLeuValAsnThrAlaGlnLeuLeuGlnPheSerLeuHisValAlaGlnGlyMet 340  
Db 1223 CGAGCCCTCGTGAACACCGCTCACTGACGTTTCTCTGTCAGCTGGGCGGAGGAGCATG 1282  
Qy 341 GlnTyrLeuGlnSerLysLysLeuValHisArgAspLeuAlaAlaAsnLleLeuVal 360  
Db 1283 GAGTACCTGGAGACAGAAAGCTGTGTACACCGGACCTGGCGCGCCGCAACATCTGTGTC 1342  
Qy 361 SerGlnAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGlnArgLysGly 380  
Db 1343 TCAGAGGACCTGGTGGCCAAAGGTCAGGACCTTGGCTGGCCAAAGCCGAGCGAGGGG 1402  
Qy 381 LeuAspSerSerArgLeuProValLysTrpThrAlaProGlnAlaLeuLysHisGlyLys 400  
Db 1403 CTGAGCTCAAGCCGGCTGGCCGTCAGTGGAGGCGGCGCGGCTGTCAACACAGG--- 1459  
Qy 401 PheThrSerLysSerAspValTrpSerPheGlyValLeuLeuTrpGlnValPheSerTyr 420  
Db 1460 TTCACGACGACAGTGGATGTCTGGAGTTTGGGGTGGTGGCTGGAGGTTCTTCANAT 1519  
Qy 421 GlnArgAlaProTyrProLysMetSerLeuLysGlnValSerGlnAlaValGlnLysGly 440  
Db 1520 GGAAGGGCTCCGTACCTAAATGTCACTGAAAGAGGTGTGAGGCGCTGGAGAGGGG 1579  
Qy 441 TyrArgMetGluProProGlnGlyCysProGlyProValHisValLeuMetSerSerCys 460  
Db 1580 TACCGCATGAAACCCCGAGAGGCTGTCCAGGCCCCCGGCGACGTCCTCATAGAGAGCTGC 1639  
Qy 461 TrpGlnLaGluProAlaArgArgProProPheArgLysLeuAlaGlnLysLeuAlaArg 480  
Db 1640 TGGGAGGACAGAGCCGCC-CCGCGGCGCAACCTTCGCAACCTGGCGAGAACCTGGCCCG 1698  
Qy 481 GlnLeuArgSerAlaGlnAlaProAlaSerValSerGlyLysAspAlaAspGlySerThr 500  
Db 1699 GAGGTACGACAGTGGAGGTGGCCCGACCTCGTCTCAGGGCGAGAGCGCAGGTGC-ACC 1757  
Qy 501 SerProArgSerGlnGluPro 507  
Db 1758 TCCGCCCGAAGCCAGAGACC 1778

RESULT 8  
US-08-604-989A-9  
: Sequence 9, Application US/08604989A  
: Patent No. 5834208  
: GENERAL INFORMATION:  
: APPLICANT: Sakano, S.  
: TITLE OF INVENTION: No. 5834208el Tyrosine Kinase  
: NUMBER OF SEQUENCES: 11  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Pennie & Edmonds LLP  
: STREET: 1155 Avenue of the Americas  
: CITY: New York  
: STATE: New York  
: COUNTRY: USA  
: ZIP: 10036-2711  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: DOS  
: SOFTWARE: FASTSEQ Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/604,989A  
: FILING DATE: February 23, 1996  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Charles E. Miller  
: REGISTRATION NUMBER: 24,576  
: REFERENCE/DOCKET NUMBER: 1920-026  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (212) 790-9090  
: TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE  
: INFORMATION FOR SEQ ID NO: 9:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1398 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: cdna to mRNA  
: ORIGINAL SOURCE:  
: ORGANISM: human  
: STRAIN: UT-7  
: US-08-604-989A-9  
Alignment Scores:  
Pred. No.: 6,65e-235  
Score: 2444.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 91.50%  
Gaps: 0  
Matches: 466  
Conservative: 0  
Mismatch: 0  
Indels: 0

US-09-977-260-2 (1-507) x US-08-604-989A-9 (1-1398)

Qy 42 MetProThrArgArgTrrAlaProGlyThrGlnCysLleThrLysCysGlnHisThrArg 61  
Db 1 ATGCCAAGAGAGCCCTGGGCGCGGACCCAGTGTATACCAATGCGAGCACACCCGC 60  
Qy 62 ProLysProGlyGlnLeuAlaPheArgLysLysValValThrLleLeuGlnAlaCys 81  
Db 61 CCCAAGCCAGGGGAGCTGGGCTTCGCCAAGGCGACGTGTGCACCATCTGGAGGCCCTGC 120  
Qy 82 GlnAsnLysSerTrpTyrArgValLysHisThrSerGlyGlnGlnGlyLeuAla 101  
Db 121 GAGAACAAAGACTGTGACCGGCTCAAGCACCAACCAATGAGACAGAGGGCTGTGCA 180  
Qy 102 AlaGlnAlaLeuArgGlnArgGlnAlaLeuSerAlaAspProLysLeuSerLeuMetPro 121  
Db 181 GCTGGGGGCTGGCGGAGCGGAGGAGCCCTCTCCGACAGCCCAAGCTCAGCTCATGCGG 240  
Qy 122 TrpPheHisGlyLysLleSerGlyGlnGlnAlaValGlnGlnLeuGlnProProGlnAsp 141  
Db 241 TGGTTCCACGGGAAGATCTCGGCGCAGGAGCTGTCCAGCTGCACCTCCCGAGAGAT 300  
Qy 142 GlnLeuPheLeuValArgGlnSerAlaArgHisProGlyAspTyrValLeuCysValSer 161  
Db 301 GGGCTGTCTCTGGTGGGAGTCCGCGGCCAACCCCGGCGACTACGTCTGTGCTGAC 360  
Qy 162 PheGlnArgAspValLleHisTyrArgValLeuHisArgAspGlnHisLeuThrLleAsp 181  
Db 361 TTGGCCGCGACGTCATCCACTACCGGCTGTGACCGCGACCGGCGCACCTCACAATCGAT 420  
Qy 182 GlnAlaValPhePheCysAsnLeuMetAspMetValGlnHisTyrSerLysAspLysGly 201  
Db 421 GAGCCCGTGTCTCTGCAACCTCATGACATGTGTGAGCATTCACGACGACAAAGAG 480  
Qy 202 AlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGlnGlu 221  
Db 481 GCTATCTGCACCAAGCTGTGACACCAAGCGGAAACACGGGACCAAGTCCGGCGAGAG 540  
Qy 222 GlnLeuAlaArgAlaGlyTrpLeuLeuAsnLeuGlnHisLeuThrLleGlnLle 241  
Db 541 GAGCTGGCGACAGGGCGGCTGTACTGAACTGCAGCATTTGACATTTGGAGCAGCATC 600  
Qy 242 GlnGlnGlyGlnPheGlnAlaValLeuGlnGlnGlyLysLysGlnLysValAlaVal 261  
Db 601 GGAAGAGGAGATTGGAGCTGTCTGAGGAGTACCTGAGGCGCAAAAGTGGCCGTG 660  
Qy 262 LysAsnLleLysCysAspValThrAlaGlnAlaPheLeuAspGluThrAlaValMetThr 281  
Db 661 AAGAATATCAAGTGTGATGTACAGCCAGGCTTTCCTGGAGCAGAGCGCCGTCAATGACG 720  
Qy 282 LysMetGlnHisGlnAsnLeuValArgLeuLeuGlnValLleLeuHisGlnGlyLeuTyr 301

Db 721 AAGATGCAACACGAGAACCTGCTGCTCTCTGCGCTGATCTCTGACCAAGGCGCTGTAC 780  
QY 302 ILevalMetGluHisValSerLysGlyAsnLeuValAsnPheLeuArgThrArgGlyArg 321  
Db 781 ATGTGATGAGGACCTGAGCAAGGAGCAACCTGTGAATCTTCTGGGACCCCGGGGTGCA 840  
QY 322 AlaLeuValAsnThrIleGlnLeuLeuGlnPheSerLeuHisValAlaGluGlyMetGlu 341  
Db 841 GCCCTGTGAAACCCCTCAGCTCCGCAAGTTTCTGTGACGTGGCCGAGGCGCATGAG 900  
QY 342 TyrLeuGluSerLysLysLeuValHisArgAspLeuAlaIleArgAsnIleLeuValSer 361  
Db 901 TACTGTGAGAGCAAGAGCTGTGACACCGGACCTGGCCCGCAACATCTCTGCTCA 960  
QY 362 GluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGluArgLysGlyLeu 381  
Db 961 GAGGACCTGTGGCCCAAGGTCACGACGACTTGTGGCTGGCCAAAGCCGAGCGAGGGGCTA 1020  
QY 382 AspSerSerArgLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLysPhe 401  
Db 1021 GACTCAAGCGCGCTGCGCCGTCAGAGTGACGGCGCCGAGGCTCTCAAAACACGGAAGTTTC 1080  
QY 402 ThrSerLysSerAspValTrpSerPheGlyValLeuLeuTrpGluValPheSerTyrGly 421  
Db 1081 ACCAGCAAGTCGAGATGCTGGAAGTTTGGGGGTCTGCTCTGGAGAGTCTTCTCATATGCA 1140  
QY 422 ArgAlaProTyrProLysMetSerLeuLysGluValSerGluAlaValGluLysGlyTyr 441  
Db 1141 CGGGCTCCGTACCCCTAAATGTCAAGAAAGAGTGTGGAGGCGCTGGAGAAAGGGGTAC 1200  
QY 442 ArgMetGluProProGluGlyCysProGlyProValHisValLeuMetSerSerCysTrp 461  
Db 1201 CGATGAAACCCCGCCAGGAGCTGTCCAGGCGCCGTCAGCTCTCATGAGCACCTCTCTG 1260  
QY 462 GluAlaGluProAlaArgArgProPheArgLysLeuAlaGluLysLeuAlaArgLys 481  
Db 1261 GAGGAGAGCCCGCCCGCGGACACCTTCCGCAAACTGGCCGAGAAAGCTGGCCGGAG 1320  
QY 482 LeuArgSerAlaGlyAlaProAlaSerValSerGlyLysAlaAspGlySerThrSer 501  
Db 1321 CTACGCAAGTCAGAGTCCCGCAGGCTCGTCTCAGGAGAGAGCCGACGAGCTCCACCTCG 1380  
QY 502 ProArgSerGlnGluPro 507  
Db 1381 CCCCAGAACGAGAGGCC 1398

RESULT 9  
US-09-741-154-1 : Sequence 1, Application US/09741154  
: Patent No. 6437110  
: GENERAL INFORMATION:  
: APPLICANT: BEASLEY, Ellen M. et al  
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
: TITLE OF INVENTION: THEREOF  
: FILE REFERENCE: CL001061  
: CURRENT APPLICATION NUMBER: US/09/741,154  
: NUMBER OF SEQ ID NOS: 4  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 1  
: LENGTH: 1713  
: TYPE: DNA  
: ORGANISM: Human  
US-09-741-154-1

Alignment Scores:  
Pred. No.: 2,16e-192 Length: 1713  
Score: 2020.50 Matches: 410  
Percent Similarity: 84.88% Conservative: 11  
Best Local Similarity: 82.66% Mismatches: 48  
Query Match: 75.65% Indels: 29  
Db: 4 Gaps: 6

US-09-977-260-2 (1-507) x US-09-741-154-1 (1-1713)  
QY 23 ProArgValSerPro-----ArgPheLeuArgAlaTrp 33  
Db 30 CCCCAGAGAGAGCGCGGGGTGGCAGAGAACACACAGCTGCAGGGGGCTGGAGAACAA 89  
QY 34 HisProProProValSerAlaArgMetProThrArgArgTrpAlaProGlyThrGlnCys 53  
Db 90 CACCCCTTCCTCC-----TCCCGCCAGAACCTGAGACCCCGGACCTCGC--- 134  
QY 54 IleThrLysCysGluHisThrArgProLysProGlyGluLeuAlaPheArgLysGlyAsp 73  
Db 135 GTTGGCGA-TGC-----TGGCGCGAGCCGGG 160  
QY 74 ValValThrIleLeuGluAlaCysGluAsnLysSerTrpIleArgValHisHisThr 93  
Db 161 TTGCTAGGCGACATTCGAGAGAGAGAAAGAAAGCTTTCATCGGTGGCTCTAGAGCATCTT 220  
QY 94 SerGlyGlnGluLysLeuAlaAlaGlyAlaLeuArgGluArgLysAla---LeuSer 112  
Db 221 AAATG-TCCCTTCATGACAGGAGCATTTCCCTGTCGACGAGAGAGAAAGGACGACCTCGGC 279  
QY 113 AlaAspProLysLeu---SerLeuMetProTrpPheHisGlyLysIleSerGlyGlnGlu 131  
Db 280 GAGGACCCGATGTCCAGACAGCATTTCTGGTGTCCAGGGAAAGATCTCGGGCCAGAG 339  
QY 132 AlaValGlnGlnLeuGlnProProGluAspGlyLeuPheLeuValArgGluSerAlaArg 151  
Db 340 GCTGTCCAGACGTCGACAGCTCCCGAGAGATGGGCTCTCTGGTGGCGGAGTCCGCGCC 399  
QY 152 HisProGlyAspTyrValLeuCysValSerPheGlyArgAspValIleHisTyrArgVal 171  
Db 400 CACCCCGGAGACTACCTCTGTGAGACTTGTGGCGGAGCTCATCCACATCCCGCTG 459  
QY 172 LeuHisArgAspGlyHisLeuThrIleAspGluAlaValPhePheCysAsnLeuMetAsp 191  
Db 460 CTGCACCGGAGCGGCACTCACAATCGATGAGGCGGTGTCTTGTGCAACCTCATAGGAC 519  
QY 192 MetValGlnHisTyrSerLysAspLysGlyAlaIleCysThrLysLeuValArgProLys 211  
Db 520 ATGTGTGAGCATTTACAGCAAGAGCAAGGGCGCATGTGACCAACAGCTGGTGAAGCAAG 579  
QY 212 ArgLysHisGlyThrLysSerAlaGluGluGluLeuAlaArgAlaGlyTrpLeuLeuAsn 231  
Db 580 CCGAAACACGGGACCAAGTCCGCCGAGAGAGAGCTGGCAGGCGGCTGTACTAGAAC 639  
QY 232 LeuGlnHisLeuThrLeuGlyAlaGlnIleGlyGluGluPheGlyAlaValLeuGln 251  
Db 640 CTGCACGATTTGACATTTGGGAGCAGATCGGAGAGAGAGTGTGAGCTGTCTGCAAG 699  
QY 252 GlyGluTyrLeuGlnLysValAlaValLysAsnIleLysCysAspValThrAlaGln 271  
Db 700 GGTGAGTACTGGGGGAAAGAGTGGCGCGAGAAATATCAAGTGTATGTGACAGCCAG 759  
QY 272 AlaPheLeuAspGluThrAlaValMetThrLysMetGlnHisGluAsnLeuValArgLeu 291  
Db 760 GCCCTCTGAGAGAGCGCGCGTCATGAGAGATGCAACAGAGAACTGTGGTGTCTTC 819  
QY 292 LeuGlyValIleLeuHisGlnGlyLeuTyrIleValMetGlnHisValSerLysGlyAsn 311  
Db 820 CTGGGCGTATCTCGACACAGGGGCTGTACATTTGTATGTAGACACTGAGCAAGGGCAAC 879  
QY 312 LeuValAsnPheLeuArgThrArgGlyArgAlaLeuValAsnThrAlaGlnLeuGln 331  
Db 880 CTGTGTAATCTTCTGGGAGACCCGGGTTCAGCCCTGTAAACACCCCTACCTCTGCAAG 939  
QY 332 PheSerLeuHisValAlaGluGlyMetGlyTyrLeuGlnSerLysLysLeuValHisArg 351  
Db 940 TTTTCTCTCAGTGGCCAGAGGAGATGAGTACTGAGAGCAAGAACTGTGGACCCGC 999  
QY 352 AspLeuAlaIleArgAsnIleLeuValSerGluAspLeuValAlaLysValSerAspPhe 371

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Dh 1000 GACGTGGCCGCCGACACATCCTGATCTCAGAGGACCTGTGTGCCCAAGTCAGCGACTTT 1059
Oy 372 GYLEuAlaLysAlaGluArgLysGlyLeuAspSerArgLeuProValLysTrpPhe 391
Dh 1060 GGCCTGGCCAAAGCCGAGGAGGAGGCTTACACTTCACGCCGCTGCCCTCAAGGAGCG 1119
Oy 392 AAlaProGluAlaLeuLysHisGlyLysPheThrSerLysSerAspValTrpSerPheGly 411
Dh 1120 GCGCCGAGGCTCTCAACACAGGAGAGTTTCCACGACAGCTGGATGTGTGAGTTGGG 1179
Oy 412 ValLeuLeuTrpGluValAlaPheSerTrpGlyArgAlaProLysProLysMetSerLeuLys 431
Dh 1180 GTGTCTCTGTGGAGGCTTCTCTCATATGAGACGGGTCTCCGTAAATATGCTCACTGAAA 1239
Oy 432 GluValSerGluAlaValAlaGluLysGlyTyrArgMetGluProProGluGlyCysProGly 451
Dh 1240 GAGGTGTGGAGGCCGTGTGAGAGGAGGATCCCATGAGACCCCGAGGGCTGTCTCAGGC 1299
Oy 452 ProValHisValLeuMetSerSerCysTrpGluAlaGluProAlaArgArgProPhe 471
Dh 1300 CCCGTGCACGTCTCATGAGCAGCTGCTGGAGGAGAGCCGCCGCCGCCGCCACCCCTTC 1359
Oy 472 ArgLysLeuAlaGluLysLeuAlaArgLysLeuArgSerAlaGlyAlaProAlaSerVal 491
Dh 1360 CGCAAACTGGCCGAGAACTGGCCCGGAGGCTACGCACTGCAAGTGCCCCCAGCCTCCGTC 1419
Oy 492 SerGlyLysAspAlaAspGlySerThrSerProArgSerGlnGluPro 507
Dh 1420 TCAGGGCGAGACCCCGACGCTCCACTCGCCCGAGACCCAGAGCCCC 1467

RESULT 10
US-09-741-154-3
: Sequence 3, Application US/09741154
: Patent No. 6437110
: GENERAL INFORMATION:
: APPLICANT: BEASLEY, Ellen M. et al
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
: FILE REFERENCE: CLO01061
: CURRENT APPLICATION NUMBER: US/09/741,154
: CURRENT FILING DATE: 2000-12-21
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 16389
: TYPE: DNA
: ORGANISM: Human
US-09-741-154-3

Alignment Scores:
Pred. No.: 1.03e-135 Length: 16389
Score: 1469.50 Matches: 501
Percent Similarity: 21.59% Conservatve: 0
Best Local Similarity: 21.59% Mismatches: 6
Query Match: 55.02% Indels: 1819
DB: 4 Gaps: 12

US-09-977-260-2 (1-507) x US-09-741-154-3 (1-16389)
Oy 1 MetaLagLysArgLysSerLeuValSerTrpArgAlaPheHisGlyCysAspSerAlaGlu 20
Dh 7229 ATGCGGGGCGAGGCTCTGTGTTCTGCGGGGCAATTTCAGGGCTGTGATTCGTCTAG 7288
Oy 21 Glu----- 21
Dh 7289 GAACCTCCCGGTAAGATCACTTCCACAGGGGCTTGGGAGGCCAGTTCTGTGGTCCC 7348
Oy 21 ----- 21
Dh 7349 ATCCAGATGCTCTGTGGGAGGCTCTCTCTGCTGCCAGCATGCCCCCACTGACCT 7408
Oy 21 ----- 21
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Dh 7409 GGGCTGGAAGTGTAGGAACGTGACCGTGGGTCCACGCCAGCTCCACCTGAGACTGT 7468
Oy 22 ---LeuProArgValSerProAlaPheLeuArgAlaTrpHisProProValSerAla 40
Dh 7469 CCCCTCCCAAGTGT-AGCCCCCGCTTCTCCGAGCCTTGACACCCCTCCCGCTCAAGCC 7527
Oy 41 ArgMetProThr----- 44
Dh 7528 AGGATGCCAACGGTAGTGTGTCTAGCCTGCTTCTCTGCTCCCGGGTCCCTTTCTTAAC 7587
Oy 44 ----- 44
Dh 7588 TCCGTCACACCTTGAGCCCTTCTCTGTAAGGGGTGTACTGTGCCCCCTACCCCTTC 7647
Oy 44 ----- 44
Dh 7648 TGCTGGCCTCGCCTGGCTTTCTCAGTCATTTGGCTTCTTGAACCTTGTGCCAGGC 7707
Oy 44 ----- 44
Dh 7708 GCCTCTCTTTGTACTACATTTCTCTGTGAGACACCCACTCCCTTTCTTTCCCCC 7767
Oy 44 ----- 44
Dh 7768 GATGTGCGTGTGTTTTCTGTGCTCTCGGCTTTTCAATCTATACCTTTCTGCC 7827
Oy 44 ----- 44
Dh 7828 TCTGTCTCTTTCCCTCCCGTCTCTGCTCCCAACATCTCGATGTCTCTCCCTTT 7887
Oy 45 ----- 45
Dh 7888 GCCCTCTCCCGGCCCTCTGCAAGAGGCTGGGCCCCGGGCAACAGTATATACCAA 7947
Oy 56 sCysGluHisThrArgProLysProGlyGluLeuAlaPheArgLysGlyAspValAlaLys 76
Dh 7948 ATGGAGACACACCGCCCAAGCAGGAGGACTGCTTCGCAAGGCGAGCGTGTAC 8007
Oy 76 rLLeuGluAlaCysGlu----- 82
Dh 8008 CATCTGTGAGGCTCTGCCA-GGTGAGAGTGCCGCGGGTGTGGCTGTGGCGCTGGGG 8066
Oy 83 -----As 83
Dh 8067 GCTCCACGAGCACACCCCAACACCCCACTTAACCCCTGCTTCTCCCTGGACAA 8126
Oy nLysSerTrpTyrArgValLysHisHisThrSerGlyGluGlyLeuLeuAlaLys 103
Dh 8127 CAAGAGCTGTACCGCGTCAGACACACACAGTGAAGAGGAGGCTGTGGCAGCTGG 8186
Oy 103 yAlaLeuArgLysGluAlaLeuSerAlaAspProLysLeuSerLeuMetPro----- 121
Dh 8187 GGCCTGTGGGAGGCGGAGGCTCTCTCGCAGACCCCAAGCTCAATGATCGGTAGT 8246
Oy 121 ----- 121
Dh 8247 GGGCAGACAGGGGCTGGGTAGGGACACCAAGTGACCCCTCCACAGCCCACT 8306
Oy 122 -----TrpPheHisGlyLysLysSerGlyGluAlaVal 133
Dh 8307 GACCAACCCCTTCGTGGCGCGCAGGTGTTCCAGGGGAAGTCTCGGCGCAGAGGCTGT 8366
Oy 133 lGlnGluLeuGlnProProGluAspGlyLeuPheLeuValArgGluSerAlaArgHisPr 153
Dh 8367 CCAGCAGCTGACGCTCCCGAGATGGCTGTCTCTGTGGGAGTCTCCGCGCCCAACC 8426
Oy 153 oGlyAspTyrValLeuCysValSerPheGlyArgAspValHisTyrArgValLeuHis 173
Dh 8427 CGCGACTACTCTGTGTGCTGTGAGCTTTGGCGGAGCTCATTCACCTTACCGGTGTGCA 8486
Oy 173 sArgAspGlyHisLeuThrHisLeuAspGluAlaValPhePheCysAsnLeuMetAspMetVal 193
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Db 8487 CCGCCAGCGCCACTCACAATGATGAGGCCGTTCTTCTGCAACCTCATGACATGGT 8546  
OY 193 1G1u----- 194  
Db 8547 GGAAGGTGCTGCCACCCAGAGGCCCCGCCGTCCTGCACTGGGGAGGCCAGGACTCC 8606  
OY 194 ----- 194  
Db 8607 GGAGACTCCCTACGTAGAGATAGAGGGGCGGTCACTGACTCCATCCCTTCCCAAGC 8666  
OY 194 ----- 194  
Db 8667 AGCTGGGCAAGACCACTCCCTACCTCTGCTGATACCCGGGACCCCTGAGCTGTGT 8726  
OY 194 ----- 194  
Db 8727 GCTTCCCAATGTGGAGATGAAGGGGTATTCCCCAGGGGCCCCCAAGGACCCCAAGGCC 8786  
OY 194 ----- 194  
Db 8787 CCCATCCCATCTCAGATGGGCAAGACAGAGACCCCAAGTATGATCCCTTAATGCA 8846  
OY 194 ----- 194  
Db 8847 GAAATAGGGGGGCTGATCCCTATGACTGCTCCCATCTACAGGTGCGCTGATCAGCTTG 8906  
OY 194 ----- 194  
Db 8907 TTCTACTCCAGGAGACTAGATGACTCTGCGGGACCCCCAGAGCCCAAGTTGAT 8966  
OY 194 ----- 194  
Db 8967 ACCAATCAGAGAGACTCCCTCTTTGGCTTGCTCCCTGCTATGAAACC 9026  
OY 194 ----- 194  
Db 9027 AGCCTTCTCTCTCCCGGTCCACCCACCCAGAGGCCACCGGGAGAGAAC 9086  
OY 195 -----H1 195  
Db 9087 AGGATCTGGGGTTCCCTCCCTGGGGGTGGGCTGATGGCTGACCATCTGAGCA 9146  
OY 195 -----H1 195  
OY 195 slyrserlysasplys[Ala]IecysrlylsleuValargProlysrlysl 215  
Db 9147 TTACACAAAGAGCAAGGGGCTATCTGCACCAAGCTGTGAGACCAAGCGMAACG 9206  
OY 215 ythrlysserAlaIgluIgluleuAlaIargAla----- 226  
Db 9207 GACCAAGTGGGCGGAGGAGGAGCTGGCCAGGGG-TAGGGAGCGCCAGAGGGGAGAGCC 9265  
OY 226 ----- 226  
Db 9266 CTTTCCCTACCCAGTTAGCCAGTCCGGGAAGGAAGGGGCTGGGGCCCCGACCTGTG 9325  
OY 226 ----- 226  
Db 9326 AGGCAGATCACCAAGCCTGTCTCCATGCCAGTATGGATAGAAGACTGGGCTGCC 9385  
OY 226 ----- 226  
Db 9386 TGGGGGTGCCACAGACACAGATCATGCTTTATTCAATAGSTCCCAAGCTTGGCACT 9445  
OY 226 ----- 226  
Db 9446 CATCTGTACATCATCACCATCTGAGCCAGAAACCTGACCCTGAACCTCCACCAACC 9505  
OY 226 ----- 226  
Db 9506 CATCTGTACATTCCTCTTGGCCAGGTTCCCAAGACCTGTGTAATCTTCTCCCTCC 9565  
OY 226 ----- 226  
Db 9566 CCTCCCAAGCCAGACTCAGAGCCCTCCCATCAGACCGGCTCTTCCCAAGAGGGGAGCT 9625

OY 226 ----- 226  
Db 9626 CCCCTTCCAGCCAGGCTTGAGTGCAGCTCAAGTTATCTTCTATCATGAACCAT 9685  
OY 226 ----- 226  
Db 9686 GCCTCCAGGAGAGAGGCCAGAGCTCCACCACTTCAGAAACCTGCCGTGAGGCTTG 9745  
OY 226 ----- 226  
Db 9746 AGCCACTTTCAGGCTCATCTGCAGAAAGCCCTTCTCCACATCCACCCCTCCAGGT 9805  
OY 226 ----- 226  
Db 9806 CAACGTGATCATGTTTTCTTCATGCTGTAGGCCATTGTATATTCTGTCTCCCTCAC 9865  
OY 226 ----- 226  
Db 9866 TGAATGCTTTTCCAGCCCTTAAGTGAATCCCAATATTTAAGTCAAAAGCAAT 9925  
OY 226 ----- 226  
Db 9926 GCCTCTTGACCCCATGCTGTCTCTTGAAGTATCTCTCTGSGGAAGTCTGTAC 9985  
OY 226 ----- 226  
Db 9986 CCATCAGGGATGATCATCAGGTGAGACTAGCATCACCTGGCCATGATCTCTTAAGAC 10045  
OY 226 ----- 226  
Db 10046 CGTGCAATTTGAGGGGGGCACTTTCTGAGAGGAGAAAGAAAGCTGCAAGACCAAG 10105  
OY 226 ----- 226  
Db 10106 AGGGCAGTGGAGGAGCAACACAGAGTGTGTTGGAGAAAGGTGAGGAGGCTAAGCCC 10165  
OY 226 ----- 226  
Db 10166 TGAATATTTGTGAACCTTATGAGTGTCCATGTGTGTTTTTCTCTGTGTGTTT 10225  
OY 226 ----- 226  
Db 10226 CTGGGGTGTGACAGGTAAAGAACTGTAGGAGAGCCAGAGGGTATTGGAGAGAC 10285  
OY 226 ----- 226  
Db 10286 AAGAGAGCCAAAGAGAAAGGAGCTTATCTGTGAGAACTGAAGTGTTCCTGGCAC 10345  
OY 226 ----- 226  
Db 10346 TACCCCTTGGGCTGACTGGAGTTCCTGGAGGCAAGTGGGGTCTGAGGGTCTCAGC 10405  
OY 226 ----- 226  
Db 10406 CAGGAGGCCCCAGCTTGACTATTTCACACACATCTCCCTCTGAAGCCCCCTTTTGT 10465  
OY 226 ----- 226  
Db 10466 TCAGTCAACGTGATAGTGTCTGTGTTGCAACAACAATAATTGTACAGAGAGTGGG 10525  
OY 226 ----- 226  
Db 10526 GTGTCTGTATATGTCTAGGGGCAATTGCCAGGCCAGAGCCACTCAATGTATGCA 10585  
OY 226 ----- 226  
Db 10586 CAGCTGCACACTGTGAGAGACATCATCTAGTCTCTCACCAAGTAAACCCCCCAATGGA 10645  
OY 227 ----- 226  
Db 10646 GGAATTAAGGGGGCCATTACCCCTGTGACTGGGTCTTCACTCCAGAGCGGGCTGTACT 10705





Db 12864 CGCAGCGAGACGCCCAACATCCCGGCCATCTCCACCCCAACAGGCGCAACCTGGT 12923  
Qy 333 IAsnPhelLeuArthrArGlyArgAlaLeuValAsnThrAlaGlnLeuLeuGlnPhse 333  
Db 12924 GAACCTTCTGGGACCGGGGTCGAGCCCTCGTGAACACCGCTCAGCTCCTCAGATTTTC 12983  
Qy 333 rLeu----- 334  
Db 12984 TCTGAAGTGGACTCTCAGGGTCTCGGGCACTGGGGTCTCGGGCGCAGATTCAG 13043  
Qy 334 ----- 334  
Db 13044 ATCCATCAAGGGGAAACTGAGCGACGGGCGAGGAGGCTTTGTGAGCTTTGGCCCCAG 13103  
Qy 334 ----- 334  
Db 13104 CACCCGAGCTTTCTGAGCCCTGAATGTGGGCATCTGGACACTGAGCCCCACGTGCC 13163  
Qy 335 -----HisValAlaGluGlyMetGluTyrLeuGlnSerLysLysLeuValH 350  
Db 13164 CTACTACCCCGACGAGCGTGGCGGAGGCGATGAGTACTGAGAGAGCTGGCCAGAGTACGC 13223  
Qy 350 IAsnAspLeuAlaAlaArGAsnIleLeuValSerGlnAspLeuValAlaLysValSerA 370  
Db 13224 ACCGCGACTGGCCCGCCGCAACATCTGTCTCAGAGAGCTGGTGGCCAGAGTACGC 13283  
Qy 370 sPheGlyLeuAlaLysAlaGluArGlyLysGlyLeuAspSerSerArgLeuProValLysT 390  
Db 13284 ACTTGGCCCTGGCCCAAGCGCGGAGGGCTAGACTCAAGCGCGGCGCCGTCAGAGT 13343  
Qy 390 rPThrAlaProGluAlaLeuLysHisGly----- 399  
Db 13344 GACGCGCGCCGAGGCTCTCAAAACAGGGGTGAGGCCCTGCTCACATACCCCTGGGCT 13403  
Qy 399 ----- 399  
Db 13404 TTGGGGTCCCCCAGCTCTGCTGTATGACCTGGGTATGTCCCTTGCCCTCTGAACT 13463  
Qy 399 ----- 399  
Db 13464 CCAGAGCAATGGCTATGCTCCCGAGNAGCTTGGCCATTAATTTGTTCTCGTAGCC 13523  
Qy 399 ----- 399  
Db 13524 CCCCTCTGGGCTCAGTTTCTCCAGCTCTGAAAAAGGCGTGGCTCAGAGACTGAAGGAA 13583  
Qy 399 ----- 399  
Db 13584 GAATTAACGAGCTTCTCTCATGCACTAAGCTAGACTAGACTCAACTGCGGGCGGCTTG 13643  
Qy 399 ----- 399  
Db 13644 GGGGAGACTCAATTAGAGAGACAGAGAGTGAAGGTCAACCCAGAGAGGCTTCTGG 13703  
Qy 399 ----- 399  
Db 13704 AGGAAGCAGGGGCTGAGCAGAAAACTGAGGGGTCTCTCACCCCGTCTCGGGCCC 13763  
Qy 400 -----LysPheThrSerLysSerAspValTTPSerPheGlyValLeuLeuTTPGluValP 418  
Db 13764 CACAGAAGTTCACGCAAGTGTCTGAGATTTTGGGTGCTGCTCTGGAGAGTCT 13823  
Qy 418 heSerTyrGlyArgAlaProTyrProLysMetSer----- 429  
Db 13824 TCTCATATGACGCGGCTCCGTACCTAAATGTG-GAGCGGGGTGCCAGGAGGACACTG 13882  
Qy 429 ----- 429  
Db 13883 GGTTCGGGCGAGTCCAGAGCTGTGGCCCTGACCCCTGCCACGCTGCTGCCAGT 13942  
Qy 430 --LeuLysGluValSerGluAlaValGluLysGlyTyrArgMetGluProProGluGlyC 449  
Db 13943 CACTGAAGAAGAGTGTGAGAGCGCGCTGAGAAAGGGGTACCGCATGTGAACCCCGCGAGGCT 14002

Qy 449 ySProGlyProValHisValLeuMetSerSerCysTTPGluAlaGluProAlaArgArp 469  
Db 14003 GTCCAGGCGCCCTGCACGCTCATGAGAGAGCTGCTGGGAGCAAGCCCCCGCCGC 14062  
Qy 469 roProPhaArgLysLeuAlaGluLysLeuAlaArgGluLeuArgSerAlaGlyAlaProA 489  
Db 14063 CACCTTCCGCAACTGGCGGAGAACTGGCCCGGAGCTACGACAGTGCAGGTGCCCGCAG 14122  
Qy 489 IAsnValSerGlyLysAspAlaAspGlySerThrSerProArgSerGlnGluPro 507  
Db 14123 CCTCGCTCAGAGGAGAGCGCGAGGCTCCACCTCGCGCCGAGAGGAGAGGCC 14178

RESULT 11  
US-08-604-989A-8  
; Sequence 8, Application US/08604989A  
; Patent No. 5834208  
GENERAL INFORMATION:  
; APPLICANT: Sakano, S.  
; TITLE OF INVENTION: No. 5834208el Tyrosine Kinase  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/604,989A  
; FILING DATE: February 23, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
; NAME: Charles E. Miller  
; REGISTRATION NUMBER: 24,576  
; REFERENCE/DOCKET NUMBER: 1920-026  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE:  
; ORGANISM: human  
; STRAIN: UT-7  
US-08-604-989A-8

Alignment Scores:  
Pred. No.: 8-81e-118 Length: 738  
Score: 1269.00 Matches: 246  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 47.51% Indels: 0  
DB: 2 Gaps: 0

US-09-977-260-2 (1-507) x US-08-604-989A-8 (1-738)

Qy 233 GlnHisLeuThrLeuGlyAlaGlnIleGlyGluGlyLupPheGlyAlaValLeuGlnGly 252  
Db 1 CAGCATTTGACATTTGGAGACAGATCGAGAGGAGATTGGAGTGTCTCTCGCAGGAT 60  
Qy 253 GluTyrLeuGlyGlnLysValAlaValLysAsnIleLysCysAspValThrAlaGlnAla 272

Db 61 GAGTACCTGGGCGAAAGGTGGCCGTGAAGAAATATCAAGTGTGAGTGAACAGCCAGCCG 120  
QY 273 PheLeuAspGluThrAlaValMetThrLysMetGlnHisGluAsnLeuValArgLeuLeu 292  
Db 121 TTCCTGGAGAGAGAGGCGCTCATGAGAGATGCAACAGAGAACTGGTGGCTTCCG 180  
QY 293 GlyAlaIleLeuHisGlnGlyLeuValIleValMetGlnHisValSerLysGlyAsnLeu 312  
Db 181 GCGGTATCTCGACACAGAGGGGTGTACATTTGTCATGAGACAGTGAAGCAAGGCAACCTG 240  
QY 313 ValAsnPheLeuArgThrArgGlyArgAlaLeuValAsnThrAlaGlnLeuGlnPhe 332  
Db 241 GTGAACCTTCTCGCGACCGGGGTGACGCTGTGTAACACCGCTACGCTCCGAGTT 300  
QY 333 SerLeuHisValAlaGluGlyMetGluTyrLeuGlnSerLysLysLeuValHisAsp 352  
Db 301 TCTCTGACGTGGCCGAGGCGCATGAGTACCTGAGAGCAAGAGCTTGTCCACCCGAC 360  
QY 353 LeuAlaAlaArgAsnIleLeuValSerGluAspLeuValAlaLysValSerAspPheGly 372  
Db 361 CTGGCGCGCGCGCAACATCTGTGTCAGAGACCTGTGGCAAGCTCAGCGACTTGGC 420  
QY 373 LeuAlaLysAlaGluArgLysGlyLeuAspSerArgLeuProValLysTrrPheAla 392  
Db 421 CTGGCGCAAGCGCGAGGGAAGGGCTAGACTCAAGCGGCTGCCCTCAAGTGGAGGGG 480  
QY 393 ProGluAlaLeuLysHisGlyLysPheThrSerLysSerAspValTrpSerPheGlyVal 412  
Db 481 CCGGAGGCTCTCAACACCGGGAAGTTCACACGACGACTCGGAGTCTGGAGTTTGGGGTG 540  
QY 413 LeuLeuTrpGluValPheSerTyrGlyArgAlaProTyrProLysMetSerLeuLysGlu 432  
Db 541 CTGCTCTGGAGGCTTTCATATGAGACGGGCTCCCTACCCCTAAATGTCACAGAAAG 600  
QY 433 ValSerGluAlaValGluLysGlyTyrArgMetGluProProGluLysProGlyPro 452  
Db 601 GTGTCGAGCGCGTGAAGGGGTACCCCATGGAACCCCGAGGCGTCCAGGCCCC 660  
QY 453 ValHisValLeuMetSerCysTrpGluAlaGluProAlaArgArgPropPheArg 472  
Db 661 GTGCACGTCCTCATGACGCTGCTGGAGGACGAGCCCGCGCGCACCTTCCCG 720  
QY 473 LysLeuAlaGluLysLeu 478  
Db 721 AAACGCGCGAGAACCTG 738  
RESULT 12  
US-07-820-011A-1  
Sequence 1, Application US/07820011A  
Patent No. 5336615  
GENERAL INFORMATION:  
APPLICANT: Bell, Leonard  
APPLICANT: Madril, Joseph A.  
APPLICANT: Warren, Stephen L.  
APPLICANT: Luthinger, Daniel J.  
TITLE OF INVENTION: Genetically Engineered  
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced  
TITLE OF INVENTION: Migration  
TITLE OF INVENTION: and Plasmidogen Activator Activity  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Maurice M. Klee  
STREET: 1951 Burr Street  
CITY: Fairfield  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06430  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb storage  
COMPUTER: IBM PC XT  
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10  
SOFTWARE: DisplayWrite 3  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/820,011A  
FILING DATE: 19920106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Klee, Maurice M.  
REGISTRATION NUMBER: 30,399  
REFERENCE/DOCKET NUMBER: LB-101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 255 1400  
TELEFAX: (203) 254 1101  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1602 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
MOLECULE TYPE: Linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Gallus, gallus  
PUBLICATION INFORMATION:  
AUTHORS: Takeya, Tatsuo  
TITLES: Structure and Sequence of the  
TITLE: Cellular Gene Homologous to the RSV src  
TITLE: Gene and the Mechanism for Generating the  
TITLE: Transforming Virus  
JOURNAL: Cell  
VOLUME: 32  
PAGES: 881-890  
DATE: March, 1983  
US-07-820-011A-1  
Alignment Scores:  
Pred. No.: 4,51e-64 Length: 1602  
Score: 737.50 Matches: 186  
Percent Similarity: 52.84% Conservative: 84  
Best Local Similarity: 36.40% Mismatches: 185  
Query Match: 27.61% Indels: 57  
DB: 1 Gaps: 15  
US-09-977-260-2 (1-507) x US-07-820-011A-1 (1-1602)  
QY 23 ProArgValSerProArgPheLeuArgAlaTrpHisProProValSerAla----- 40  
Db 137 CCCCAGCCGCTCT-----TTGGACCGTGGCCACCGACCTCTTGGGGGCT 190  
QY 41 -----ArgMetProThrArgArg-----TrpAlaProGly---- 50  
Db 191 TCACACCTCTGACACCGCTTACCTGCCCGCAGCGTCCGGGCGACGCGTGC-GGCGTC 249  
QY 51 ThrGlnCysIleThrLysCysGlnHisThrArgProLysProGlyLysLeuAlaPheArg 70  
Db 250 ACCACTTGTGGCTCTACGACTCAGTCCGAGTCCCGAGCTGAAGCGACTTGTCTTCAG 309  
QY 71 LysGluAspValAlaThrIleLeuGluAlaCysGluAsnLysSerTrpTyrArgValLys 90  
Db 310 AAAGAGAACGCTCGAGATGTCAACAAACACGGAAGGT-----GACTGGTGGCTGCAT 366  
QY 91 HisHisThrSerGlnGlnGluLeuLeuAlaIleGlyAlaLeuArgGluArgGluAla 110  
Db 367 TCCCTCATAAGAGACAGAGCGGCTACATCCCGAGTAATATGCGCGGCTCAGACTCC 426  
QY 111 LeuSerAlaAspProLysLeuSerLeuMetProTrrPheHisGlyLysIleSerGlyGln 130  
Db 427 ATCCAGGCTGAA-----GAGTGTACTTGGGGAAGATCACTCGTCGG 468  
QY 131 GluAlaValGlnGlnLeuGlnProProGluAsp-----GlyLeuPheLeuValArgGlu 148  
Db 469 GAGTCCGAGCGGCTGTCTCAACCCCGAAACCCCGGGGAACTTCTTGGTCCGGAG 528  
QY 149 SerAlaArgHisProGlyAspTyrValLeuCysValSer-----PheGly 163

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Db      529 AGCGAGACGACAAAGGTGCTATTGCTCTCCGTTTCTGACTTTGACACGCCAGGGG 588
Oy      164 ArgAspValIleHisThrArgValLeuHisArgAsp---GlyHisLeuThrIleAspGlu 182
Db      589 CTCATGTGAGCACTACAGATCGCAAGTCGACAGCGGGGCTTCTACTATCACCTCA 648
Oy      183 AlaValPhePheCysAsnLeuMetAspMetValGluHisThrSerLysAspLysGlyAla 202
Db      649 CGCACACAGTTCAGCAGCTGACGAGCTGAGGCTTACTACTCAACATGCTGATGCG 708
Oy      203 IleCysThrLysLeu-----ValArgProLysArgLysHisGlyThrLysSerIleGlu 220
Db      709 TTGTCCACCGCTTACCAAGCTCTGCCCCACGTCCAGCCCAAGCCAGAGGGA----- 762
Oy      221 GluGluLeuAlaArgAlaGlyThrLeuLeuAsnLeuGlnHisLeuThrLeuGlyAlaGln 240
Db      763 -----CTGCCCAAGAGCGCGTGGGAATCCCGCGAGTGGCTCGGCTGGAGGTGAG 816
Oy      241 IleGlyGluGlyGluPheGlyAlaValLeuGlnGlyGlyThrLeuGly---GlnLysVal 259
Db      817 CTGGGGCAGGGCTGCTTGGAGAGGTCTGATGGGACCTGGACGCGCACACAGAGCTG 876
Oy      260 AlaValLysAsnIleLys---CysAspValThrIleGlnIlePheLeuAspGluThrAla 278
Db      877 GCCATTAAGACTCTGAAGCCCGGCAACATGTCCCGAGGCGCTTCTCGAGAGAGCCCA 936
Oy      279 ValMetThrLysMetGlnHisGluAsnLeuValArgLeuGlyValIleLeuHisGln 298
Db      937 GTGATGAAGAAGCTCGCGCATGAGAAAGCTGGTTCAGCTGTACGCGAGTGGTGTGGAA 996
Oy      299 GlyLeuThrIleValMetGlnHisValSerLysGlyAsnLeuValAsnPheLeuArgThr 318
Db      997 CCCATCTACATCGTCACTAGTACATGAGCAAGGGGAGCTCTTGATTTCTCTGAAGGA 1056
Oy      319 ArgGlyArgAlaLeuValAsnThrAlaGlnLeuGlnPheSerLeuHisValAlaGlu 338
Db      1057 GAGATGGCAAGTACCTCGGCTGCCACAGCTCGTCGATATGGCTGCTCAAGTTTCACCC 1116
Oy      339 GlyMetGluThrLeuGluSerLysLysLeuValHisArgAspIleAlaIleArgAsnIle 358
Db      1117 GGCATGGCCCTATGTGGAGAGATGAACTAGTGCACGACGACCTCGGCGGCCCAACTC 1176
Oy      359 LeuValSerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAla----- 376
Db      1177 CTGTGGGGGAGAACCTGTGTGCAGAGTGGCTGCTTGGGTCGACCGCTCATCGAG 1236
Oy      377 -----GluArgGlyGlyLeuAspSerSerArgLeuProValLysThrThrAlaProGlu 394
Db      1237 GACAAACGAGTACACAGCAGCGCAAGGTCCAAAGTTCCCATCAAGTGAACAGCCCGAG 1296
Oy      395 AlaLeuLysHisGlyLysPheThrSerLysSerAspValIlePheSerPheGlyValLeuLeu 414
Db      1297 GCAGCCCTCTATGGCGGGTTCACCATCAAGTCGATGTCGTGCTTGGCATCTGCTG 1356
Oy      415 TrpGluValPheSerThrGlyArgAlaProGlyTrpLysMetSerLeuLysGluValSer 434
Db      1357 ACTGAGCTGACCAACGAGCGCGGGTGCATACCCAGGAGGTCACAAAGGAGAGTCTG 1416
Oy      435 GluAlaValGluLysGlyThrArgMetGluProProGluGlyCysProGlyProValHis 454
Db      1417 GACCAAGGTGAGAGGGGCTACCGCATGCGCTGCCCGCGCGAGTCCGAGTCCGTGAT 1476
Oy      455 ValLeuMetSerSerCysTrpGluAlaGluProAlaArgArgProProPheArgLysLeu 474
Db      1477 GACCTCATGTGCCAGTGTCTGGCGGAGGAGACCTGAGAGCGCGCCACTTTTGATGACTG 1536
Oy      475 AlaGluLysLeuAlaArgGluLeuArgSerAlaGlyAlaProAlaSerValSerGlyGln 494
Db      1537 CAGGCTTCTCTG-----GAG 1551
Oy      495 AspAlaAspGlySerThrSerProArgSerGln 505

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Db      1552 GACTACTTACCTCGACAGAGCCCGCATACCAG 1584
RESULT 13
PCT-US93-00445-1
Sequence 1, Application PC/TUS9300445
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madril, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 760 Kb storage
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/820,011
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-101PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1602 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANNT-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV SRC
TITLE: Gene and the Mechanism for Generating the
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
PCT-US93-00445-1
Alignment Scores:
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DB: 5 Gaps: 15
US-09-977-260-2 (1-507) x PCT-US93-00445-1 (1-1602)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd

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Gapop 10.0 , Gapext 1.0

Searched: 1632420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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4	1930	96.5	1989	14	US-10-084-817-341	Sequence 341, Appl1
5	1377	68.8	1713	12	US-10-187-900-1	Sequence 1, Appl1
6	547.6	27.4	2187	10	US-09-954-531-188	Sequence 188, Appl1
7	547.6	27.4	2187	15	US-10-298-377A-1	Sequence 1, Appl1
8	547.6	27.4	2420	14	US-10-177-233-87	Sequence 8, Appl1
9	455	22.8	16389	12	US-10-187-900-3	Sequence 3, Appl1
10	192.6	9.6	2015	10	US-09-954-456-1983	Sequence 1983, Appl1
11	192.6	9.6	2015	14	US-10-007-010-3	Sequence 3, Appl1
12	191.4	9.6	5537	10	US-09-880-107-3710	Sequence 3710, Appl1
13	186.2	9.3	1911	10	US-09-917-800A-1611	Sequence 1611, Appl1
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21	165.8	8.3	2674	13	US-10-003-295-1	Sequence 1, Appl1
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44	133	6.7	2129	12	US-09-960-706-954	Sequence 954, Appl1
45	132.8	6.6	4658	9	US-09-895-652-1	Sequence 1, Appl1

## ALIGNMENTS

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RESULT 1
US-09-977-269-1
: Sequence 1, Application US/09977269
: Patent No. US20020082037A1
: GENERAL INFORMATION:
: APPLICANT: ULLRICH, AXEL
: APPLICANT: GISHIZKY, MIKHAIL
: APPLICANT: SURES, IRMINGARD
: TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
: FILE REFERENCE: 038602/1260
: CURRENT APPLICATION NUMBER: US/09/977,269
: CURRENT FILING DATE: 2001-10-16
: PRIOR APPLICATION NUMBER: 08/732,545
: PRIOR FILING DATE: 1994-04-22
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Unknown Organism
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (258)..(1778)
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
: OTHER INFORMATION: kinase 1
US-09-977-269-1

Query Match          100.0%; Score 2000; DB 9; Length 2000;
Best Local Similarity 100.0%; Pred. No.:0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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 : APPLICANT: GISHIZKY, MIKHAIL  
 : APPLICANT: SURES, IRMINARD  
 : TITLE OF INVENTION: NOVEL MEKKAROCYTIC PROTEIN TYROSINE KINASES  
 : FILE REFERENCE: 038602/1260  
 : CURRENT APPLICATION NUMBER: us/09/977,260  
 : PRIOR APPLICATION NUMBER: 2001-10-16  
 : PRIOR FILING DATE: 1994-04-22  
 : NUMBER OF SEQ ID NOS: 24  
 : SOFTWARE: PatentIn Ver. 2.1

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US-09-977-260-1

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DB 841 ATTACAGCAAGACAAAGGGCGCTATCTGACCAAGCTGCTGAGACCAAGCGGAACAGC 900  
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DB 901 GGACCAAGTCCGCGGAGAGAGCTGCGCAGGGGGGCTGTTACTGAACCTGACGACTT 960  
OY 961 TGACATTGGGAGACAGATCCGAGAGGAGAGGATTTGAGAGCTGTCTGAGGGGTGATACC 1020  
DB 961 TGACATTGGGAGACAGATCCGAGAGGAGAGGATTTGAGAGCTGTCTGAGGGGTGATACC 1020  
OY 1021 TGGGCAAAAGGTGCGCTGAGAAATATCAAGTGTGATGACACAGCCAGGCTTCTCTG 1080  
DB 1021 TGGGCAAAAGGTGCGCTGAGAAATATCAAGTGTGATGACACAGCCAGGCTTCTCTG 1080  
OY 1081 ACGAGACGGCGCTCATGACGAAGATGCAACAGAGACCTGTGTCTCTGAGGCTGGA 1140  
DB 1081 ACGAGACGGCGCTCATGACGAAGATGCAACAGAGACCTGTGTCTCTGAGGCTGGA 1140  
OY 1141 TCTGACACAGGGGGCTGACATTTGTATGAGAGACAGTGAAGGGAACCTGGTGAAGT 1200  
DB 1141 TCTGACACAGGGGGCTGACATTTGTATGAGAGACAGTGAAGGGAACCTGGTGAAGT 1200  
OY 1201 TTTCTGGAGACCGGGGGGTGAGAGCTCTGTAACACCGCTCAGCTCCTGCAAGTTTCTCTG 1260  
DB 1201 TTTCTGGAGACCGGGGGGTGAGAGCTCTGTAACACCGCTCAGCTCCTGCAAGTTTCTCTG 1260  
OY 1261 ACGTGGCCGAGGGCATGAGATACCTGAGAGACAGAGCTTGTGACACCGGCACTGGGCG 1320  
DB 1261 ACGTGGCCGAGGGCATGAGATACCTGAGAGACAGAGCTTGTGACACCGGCACTGGGCG 1320  
OY 1321 CCCGCAATCCTGCTCAGAGGACCTGGTGGCCAAAGTTCAGGCACTTTGGGCTGGGCA 1380  
DB 1321 CCCGCAATCCTGCTCAGAGGACCTGGTGGCCAAAGTTCAGGCACTTTGGGCTGGGCA 1380  
OY 1381 AAGCCGAGCGAAGGGGCTAGACTCAAGCCGGCTCCCGTCAAGTGAAGAGGCGCCGAGG 1440  
DB 1381 AAGCCGAGCGAAGGGGCTAGACTCAAGCCGGCTCCCGTCAAGTGAAGAGGCGCCGAGG 1440  
OY 1441 CTCTCAAAACAGGGGAATTCACACAGCAAGTGGATGTCTGAGATTTTGGGGTGTCTCT 1500  
DB 1441 CTCTCAAAACAGGGGAATTCACACAGCAAGTGGATGTCTGAGATTTTGGGGTGTCTCT 1500  
OY 1501 GGGAGGCTTTCATATGAGAGGGGCTCCGTAACCTTAATGTCACTGAAGAGGTGGG 1560  
DB 1501 GGGAGGCTTTCATATGAGAGGGGCTCCGTAACCTTAATGTCACTGAAGAGGTGGG 1560  
OY 1561 AGGCGGTGAGAAAGGGGTACCGCATGGAACCCCGGAGGGGCTGTCCAGGCCCGCTGAC 1620  
DB 1561 AGGCGGTGAGAAAGGGGTACCGCATGGAACCCCGGAGGGGCTGTCCAGGCCCGCTGAC 1620  
OY 1621 TCCTCATGACAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
DB 1621 TCCTCATGACAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
OY 1681 TCTCATATGAGAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740  
DB 1681 TCTCATATGAGAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740  
OY 1741 ACGGCAAGCTGAG 1800  
DB 1741 ACGGCAAGCTGAG 1800  
OY 1801 TGGGCAAG 1860  
DB 1801 TGGGCAAG 1860  
OY 1861 AGGCTCAGAGGGGGGAG 1920  
DB 1861 AGGCTCAGAGGGGGGAG 1920  
OY 1921 GGGCTGAGGGGGGGGAG 1980  
DB 1921 GGGCTGAGGGGGGGGAG 1980

Db 1921 GGCTGTGGGCGCCGTGGAGACCCAGACCTGCGAAGATGATCGCCCGATAAAGACGG 1980  
Qy 1981 ATTCTAAGACTCTAAAAA 2000  
1981 ATTCTAAGACTCTAAAAA 2000

## RESULT 3

US-09-977-261-1

; Sequence 1, Application US/09977261

; Publication No. US20030054527A1

; GENERAL INFORMATION:

; APPLICANT: ULLRICH, AXEL

; APPLICANT: GISHIZKY, MIKHAIL

; APPLICANT: SURES, IRMINGARD

; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES

; FILE REFERENCE: 038602/1259

; CURRENT APPLICATION NUMBER: US/09/977, 261

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 08/232, 545

; PRIOR FILING DATE: 1994-04-22

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2000

; TYPE: DNA

; ORGANISM: Unknown Organism

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (258)..(1778)

; FEATURE: OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte

; OTHER INFORMATION: kinase 1

; US-09-977-261-1

Query Match 100.0%; Score 2000; DB 11; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGTCAAGTTGTGCAGCGCGGACCGCTCGGGGTGTGCAGCGCGCTCGGAGGCCC 60  
Db 1 CTGCGTCAAGTTGTGCAGCGCGGACCGCTCGGGGTGTGCAGCGCGCTCGGAGGCCC 60  
Qy 61 TCCTGG 120  
Db 61 TCCTGG 120  
Qy 121 AGGCTGGGTCCATGTGGCAGCCAGCTCCCTACCTCTCTGTGCGAGCGCGCTGTGGCA 180  
Db 121 AGGCTGGGTCCATGTGGCAGCCAGCTCCCTACCTCTCTGTGCGAGCGCGCTGTGGCA 180  
Qy 181 GGCCATTCCAGCGTCCCGACCTGTGACCACTTGTCTGAGTGTCTCTACCTGTCCCTCAG 240  
Db 181 GGCCATTCCAGCGTCCCGACCTGTGACCACTTGTCTGAGTGTCTCTACCTGTCCCTCAG 240  
Qy 241 TTTTCCTCTGCGGGGGGAGTGGCGGGGGGAGGCTCTGTGTTTCTGTGGCGGGATTTCACG 300  
Db 241 TTTTCCTCTGCGGGGGGAGTGGCGGGGGGAGGCTCTGTGTTTCTGTGGCGGGATTTCACG 300  
Qy 301 GGTGTATTCTGTGTGAGAACTTCCCGGGGTGAGCCCCCGCTTCTCCGAGCTGGGACG 360  
Db 301 GGTGTATTCTGTGTGAGAACTTCCCGGGGTGAGCCCCCGCTTCTCCGAGCTGGGACG 360  
Qy 361 CCCCTCCGCTCTCAGCAGAGATGCAACGAGGGGTGGGCGCGGGACCCAGCATGTATCA 420  
Db 361 CCCCTCCGCTCTCAGCAGAGATGCAACGAGGGGTGGGCGCGGGACCCAGCATGTATCA 420  
Qy 421 CCAATGTGAGCAGACCCCGCCCAAGCCAGGGAGGTGGCTTCCGAAAGGGAGCTGG 480  
Db 421 CCAATGTGAGCAGACCCCGCCCAAGCCAGGGAGGTGGCTTCCGAAAGGGAGCTGG 480  
Qy 481 TCACCATCTCTGAGGGCTGTGAGAACAGAGCTGTACCGGTCAAGACACACACAGTGS 540  
Db 481 TCACCATCTCTGAGGGCTGTGAGAACAGAGCTGTACCGGTCAAGACACACACAGTGS 540

Db 481 TCACCATCTCTGAGGGCTGTGAGAACAGAGCTGTACCGGTCAAGACACACACAGTGS 540  
Qy 541 GACAGAGAGGGGCTGTGGCAGCTTGGGGGCTGGCGGAGCGGAGGCGCTCTCCGACAGCC 600  
Db 541 GACAGAGAGGGGCTGTGGCAGCTTGGGGGCTGGCGGAGCGGAGGCGCTCTCCGACAGCC 600  
Qy 601 CCAAGCTCAGCTTCATGCGCTGTGTCCACGGGAAGATCTCGGGGACAGAGGCTGTCCAGC 660  
Db 601 CCAAGCTCAGCTTCATGCGCTGTGTCCACGGGAAGATCTCGGGGACAGAGGCTGTCCAGC 660  
Qy 661 AGCTGCAGCTCCCGAGAGATGGGCTGTCTCTGTGTGGGAGATCCGGCGCCACCCCGCG 720  
Db 661 AGCTGCAGCTCCCGAGAGATGGGCTGTCTCTGTGTGGGAGATCCGGCGCCACCCCGCG 720  
Qy 721 ACTACGTCTGTGTGTGAGCTTTTGGCGGACGTCATCTACCTACCGGCTGTGACCGCG 780  
Db 721 ACTACGTCTGTGTGTGAGCTTTTGGCGGACGTCATCTACCTACCGGCTGTGACCGCG 780  
Qy 781 ACGGCCACCTCAGCAATGATGAGGCGGTGTCTTCTGCAACCTTCATGAGATGGTGGAGC 840  
Db 781 ACGGCCACCTCAGCAATGATGAGGCGGTGTCTTCTGCAACCTTCATGAGATGGTGGAGC 840  
Qy 841 ATTACAGCAGAGCAAGGGGCTATCTGCACCAAGCTGTGTGAGACCAAAAGCGAAACAGC 900  
Db 841 ATTACAGCAGAGCAAGGGGCTATCTGCACCAAGCTGTGTGAGACCAAAAGCGAAACAGC 900  
Qy 901 GGACCAAGTGGCGGAGAGAGCTGGCGCAGGGGCGCTGTTACTTAACCTGACAGATT 960  
Db 901 GGACCAAGTGGCGGAGAGAGCTGGCGCAGGGGCGCTGTTACTTAACCTGACAGATT 960  
Qy 961 TGACATTGGGAGCAGAGATGCGAGAGAGAGTTTGGAGCTGTCTGACAGGTTGAGTACC 1020  
Db 961 TGACATTGGGAGCAGAGATGCGAGAGAGAGTTTGGAGCTGTCTGACAGGTTGAGTACC 1020  
Qy 1021 TGGGGCAAAAGTGTGCGCTGTAAGATATCAAGTGTGTGTGACAGCCGACCTTCTCTGG 1080  
Db 1021 TGGGGCAAAAGTGTGCGCTGTAAGATATCAAGTGTGTGTGACAGCCGACCTTCTCTGG 1080  
Qy 1081 ACGAGAGCGGCGTATGACGAAGATGCAACACAGCAAGCTGTGCGCTCTCTGGCGTGA 1140  
Db 1081 ACGAGAGCGGCGTATGACGAAGATGCAACACAGCAAGCTGTGCGCTCTCTGGCGTGA 1140  
Qy 1141 TCCTGCACAGGGGCTGTATCTGTATGTAGAGCAGTGTGAGCAAGGGCAACTGTGTA 1200  
Db 1141 TCCTGCACAGGGGCTGTATCTGTATGTAGAGCAGTGTGAGCAAGGGCAACTGTGTA 1200  
Qy 1201 TTTCTGGGAGACCGGGGGTGTGAGCCCTGTGTGAACCGCTGTGACGCTCTGCAATTTCTCTGC 1260  
Db 1201 TTTCTGGGAGACCGGGGGTGTGAGCCCTGTGTGAACCGCTGTGACGCTCTGCAATTTCTCTGC 1260  
Qy 1261 ACGTGGCGAGGCGATGAGTACCTGTGAGAGCAAGAGCTTGTGCAACCGGACCTGGCCG 1320  
Db 1261 ACGTGGCGAGGCGATGAGTACCTGTGAGAGCAAGAGCTTGTGCAACCGGACCTGGCCG 1320  
Qy 1321 CCCGCAACATCTGTGTCTCAGAGAGCTGTGTGCGCAAGTGTGACGACTTTGGCTTGCCA 1380  
Db 1321 CCCGCAACATCTGTGTCTCAGAGAGCTGTGTGCGCAAGTGTGACGACTTTGGCTTGCCA 1380  
Qy 1381 AAGCGGAGGGAAGGGGCTGAGCTCAAGCGGGGCGCCGCTCAAGTGTGAGAGCGGCGGAGG 1440  
Db 1381 AAGCGGAGGGAAGGGGCTGAGCTCAAGCGGGGCGCCGCTCAAGTGTGAGAGCGGCGGAGG 1440  
Qy 1441 CTCTCAAAACAGGGAAGTTTACCAAGCAAGTGTGTGAGTGTGTGGGGTGTGCTGT 1500  
Db 1441 CTCTCAAAACAGGGAAGTTTACCAAGCAAGTGTGTGAGTGTGTGGGGTGTGCTGT 1500  
Qy 1501 GGGAGGCTTCTCATATGAGCGGGCTCCGATACCTTAATGTCACTGAAAGAGTGTGG 1560  
Db 1501 GGGAGGCTTCTCATATGAGCGGGCTCCGATACCTTAATGTCACTGAAAGAGTGTGG 1560  
Qy 1561 AGGCGGTGTGAGAGGGGTACCGATGAGAACCCCGCGAGGGCTGTCCAGGCGCGTGCAGC 1620  
Db 1561 AGGCGGTGTGAGAGGGGTACCGATGAGAACCCCGCGAGGGCTGTCCAGGCGCGTGCAGC 1620



Db 1260 GCACGTGGCCGAGGCGATGAGTACCTGGAAGCAAGAAAGCTTGTGCACCCGCGACTGGC 1319  
QY 1319 CGCCCGCAACATCTGGTCTCAGAGAGACCTGTGGCCCAAGTGCAGGACTTTGGCCGTGGC 1378  
Db 1320 CGCCCGCAACATCTGGTCTCAGAGAGACCTGTGGCCCAAGTGCAGGACTTTGGCCGTGGC 1379  
QY 1379 CAAGCGCGAGGAGGAGGAGGAGTACCTCAAGCCGGCTGGCCGTCAAGTGCAGGAGGAGGAGG 1438  
Db 1380 CAAGCGCGAGGAGGAGGAGGAGTACCTCAAGCCGGCTGGCCGTCAAGTGCAGGAGGAGGAGG 1439  
QY 1439 GGCCTCAACACAGGAGGAGTACCTCAAGCCGGCTGGCCGTCAAGTGCAGGAGGAGGAGGAGG 1498  
Db 1440 GGCCTCAACACAGGAGGAGTACCTCAAGCCGGCTGGCCGTCAAGTGCAGGAGGAGGAGGAGG 1499  
QY 1499 CTGGGAGGTCTTCTCATATGAGAGGAGGAGTACCTCAAGCCGGCTGGCCGTCAAGTGCAGG 1558  
Db 1500 CTGGGAGGTCTTCTCATATGAGAGGAGGAGTACCTCAAGCCGGCTGGCCGTCAAGTGCAGG 1559  
QY 1559 GGAAGCGGTGGAGAGGAGGAGTACCTCAAGCCGGCTGGCCGTGGTGCAGGAGGAGGAGGAGG 1618  
Db 1560 GGAAGCGGTGGAGAGGAGGAGTACCTCAAGCCGGCTGGCCGTGGTGCAGGAGGAGGAGGAGG 1619  
QY 1619 GGTCTCATGAGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1678  
Db 1620 GGTCTCATGAGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1678  
QY 1679 GGCCTGAGAGGAGGAGGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1738  
Db 1679 GGCCTGAGAGGAGGAGGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1738  
QY 1739 GGAAGCGGTGGAGAGGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1797  
Db 1739 GGAAGCGGTGGAGAGGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1797  
QY 1798 CCTTGGCCCGAGAGGAGGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1857  
Db 1798 CCTTGGCCCGAGAGGAGGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1857  
QY 1858 AGGAGGAGGAGGAGGAGGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1917  
Db 1858 AGGAGGAGGAGGAGGAGGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1917  
QY 1918 GGGGAGGAGGAGGAGGAGGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1977  
Db 1918 GGGGAGGAGGAGGAGGAGGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1977  
QY 1978 CGGATTTCAAG 1989  
Db 1978 CGGATTTCAAG 1989

RESULT 5  
US-10-187-900-1  
; Sequence 1, Application US/10187900  
; Publication No. US20030166221A1  
; GENERAL INFORMATION:  
; APPLICANT: BEASLEY, Ellen M. et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001061  
; CURRENT APPLICATION NUMBER: US/10/187,900  
; CURRENT FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1713  
; TYPE: DNA  
; ORGANISM: Human  
US-10-187-900-1  
Query Match 68.8%; Score 1377; DB 12; Length 1713;  
Best Local Similarity 99.3%; Pred. No. 0;

Matches 1383; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 608 CAGCTCATAGCCGTGGTTCACAGGAGAGATCTCGGGCCAGAGAGGTCTGCAGCAGCTGCA 667  
Db 297 CAGCAGCTTCTGTGGTTCACAGGAGAGATCTCGGGCCAGAGAGGTCTGCAGCAGCTGCA 356  
QY 668 GCGTCCCGAGAGATGGCTGTCTGTGGTGGAGAGTCCGGGCGCCACCCGGGAGCTACGT 727  
Db 357 GCGTCCCGAGAGATGGCTGTCTGTGGTGGAGAGTCCGGGCGCCACCCGGGAGCTACGT 416  
QY 728 CCGTGGCGAGGAGTGGTGGCGGAGGAGTCCAGTCCAGGAGTCCAGCAGGAGGAGGAGGAG 787  
Db 417 CCGTGGCGAGGAGTGGTGGCGGAGGAGTCCAGTCCAGGAGTCCAGCAGGAGGAGGAGGAG 476  
QY 788 CCGTCAACATGATGAGGAGGAGTGGTGGCGGAGGAGTCCAGTCCAGGAGTCCAGCAGGAGGAG 847  
Db 477 CCGTCAACATGATGAGGAGGAGTGGTGGCGGAGGAGTCCAGTCCAGGAGTCCAGCAGGAGGAG 536  
QY 848 CAAGGACAAAGGCGCTATCTGCACCAAGTGGTGAACCAAGCGCAAGCGGAGGAGGAGGAGGAG 907  
Db 537 CAAGGACAAAGGCGCTATCTGCACCAAGTGGTGAACCAAGCGGAGGAGGAGGAGGAGGAGGAG 596  
QY 908 GTGGGCGGAGGAGGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 967  
Db 597 GTGGGCGGAGGAGGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 656  
QY 968 GGGAGGACAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1027  
Db 657 GGGAGGACAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 716  
QY 1028 AAAGGTGGCGGTGAAGATATCAAGTGTGATGTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1087  
Db 717 AAAGGTGGCGGTGAAGATATCAAGTGTGATGTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 776  
QY 1088 GGGCGGTATGAGCAAGATGCAACAGAGAACTGGTGGCGTCTCGAGGAGTACCTGGAGGAGGAG 1147  
Db 777 GGGCGGTATGAGCAAGATGCAACAGAGAACTGGTGGCGTCTCGAGGAGTACCTGGAGGAGGAG 836  
QY 1148 CCAAGGAGGAGTATGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1207  
Db 837 CCAAGGAGGAGTATGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 896  
QY 1208 GAGCCGGGAGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1267  
Db 897 GAGCCGGGAGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 956  
QY 1268 CGAGGAGGAGTATGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1327  
Db 957 CGAGGAGGAGTATGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1016  
QY 1328 CATCTGTGTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1387  
Db 1017 CATCTGTGTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1076  
QY 1388 GCGGAGGAGGAGTATGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1447  
Db 1077 GCGGAGGAGGAGTATGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1136  
QY 1448 ACAGGAGGAGTATGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1507  
Db 1137 ACAGGAGGAGTATGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1196  
QY 1508 CTCTCTCATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1567  
Db 1197 CTCTCTCATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1256  
QY 1568 GGAAGAGGAGTATGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1627  
Db 1257 GGAAGAGGAGTATGATGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1316  
QY 1628 GAGCAGCTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1687  
Db 1317 GAGCAGCTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1376









APPLICANT: Meyers, Rachel E.  
APPLICANT: Bast Jr., Robert C.  
APPLICANT: Hortobagyi, Gabriel N.  
APPLICANT: Puzstai, Lajos  
APPLICANT: Meric, Funda  
APPLICANT: Sahin, Aysegul  
APPLICANT: Mills, Gordon B.  
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,  
FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER  
CURRENT APPLICATION NUMBER: US/10/177,293  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: US 60/299,887  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: US 60/301,572  
PRIOR FILING DATE: 2001-06-27  
PRIOR APPLICATION NUMBER: US 60/306,501  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: US 60/325,002  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: US 60/362,585  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/xxx,xxx  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 87  
LENGTH: 2420  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-177-293-87

Query Match 27.4%: Score 547.6; DB 14; Length 2420;  
Best Local Similarity 64.9%: Pred. No. 8.3e-124;  
Matches 846; Conservative 0; Mismatches 449; Indels 9; Gaps 2;

QY 395 CTGGGCCCCGGGACCCAGTGTATACCAATGCGAGCACGCCGCCCAAGCCAGGGGA 454  
DB 433 CTGGCATCCGCTGACAGATGTATTGGCAAGTACACTCCACGCACTGCCAGAGGA 492  
QY 455 GCTGGCTTCCGCAAGGGGACGCTGTCACCATCTGAGGCGCTCGAGAACAGAGCTC 514  
DB 493 CTTGCTTCTGCAAGAGAGAGCTGCTACCATTTGTGCGCTACCAAGGACCCCACTG 552  
QY 515 GTACCGGCTCAAGACCAACCACTGAGAGAGGGGCTGTGAGCTGGGGGCTGGC 574  
DB 553 GTCAAGGCCA---AAAACAAGGTGGGGCGGTGAGGGCATCTCCAGCACTACGTCCA 609  
QY 575 GGAGCGGAGGCGCTCTCCGAGACCCCAAGCTCAGCTCATGCGGTTCACAGGGA 634  
DB 610 GAACGGGAGGGCGTGAAGGGGGGTACCAAACTCAGCTCATGCTTGGTTCCAGGCA 669  
QY 635 GATCTGGGCGCAAGAGGCTGTCCAGCACTGACCTCCCGAGATGGGCTTCTCGT 694  
DB 670 GATACACAGGGAGAGGCTGAGCGGCTTGTACCCCGGAGACAGGCTGTCTGCT 729  
QY 695 GCGGAGATCCGCGGCGCACCCCGGAGCTACGCTGCTGAGCTTTGGCGCGAGCT 754  
DB 730 GCGGAGAGAGCAACACACACCCCGGAGACTACAGCTGTGCTGAGCTCGCAGCGCAAGT 789  
QY 755 CATCCACTACCGCTGTGTGACCGCGAGCGGCACTCAATCATGATGAGCGGCTTCTT 814  
DB 790 GAGACACTACCGCATGTACATGTCAGCAAGCTCAGCATGACAGGAGGTACTT 849  
QY 815 CTGCAACCTCATGACATGTGTGAGCATTTACAGCAAGGAGGCGCTATCTACACAA 874  
DB 850 TGAGAACCTCATGAGTGTGTGAGAGCACTACACCTCAGACCAATGAGACTGTACGCG 909  
QY 875 GCTGGTGAAGCAAGCGGAAACAGGGAGCAAGTGGCGAGGAGGAGGCGGCGAGGCG 934  
DB 910 CTTATTTAAACCAAGGTGATGAGGAGCAGAGTGGCGGCCAGATGATGTTCTACCGCAG 969  
QY 935 GGGCTGTTACTGAACCTGACAGATTGACATTGGAGACAGATCGAGAGGAGAGATT 994

DB 970 CGGCTGGGCGCTGAACATGAAGAGAGCTGACAGTCTCAGACCATCGGAGGGGAGATT 1029  
QY 995 TGGAGCTGTCTGAGAGGTGAGTACCTGGGGCAAAAGCTGGCGGTGAAGATATCAAGTG 1054  
DB 1030 CGGAGAGTATGTGTGGCCATTAACGAGGAAACAAAGTGGCTCAAGTGAATGAAGAA 1089  
QY 1055 TGAGTGAACAGCCAGGCGCTTCTGAGAGAGAGCGGCTCATGATGACGAAGATGCAACGA 1114  
DB 1090 CGAGCCAGCTGCGGCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1149  
QY 1115 GAACCTGTGTGCTGCTGAGGCGGTGATCTGACACAG-----GGCTGATATTTGTCAT 1168  
DB 1150 CAACCTGTGACAGCTCTGAGGCGGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1209  
QY 1169 GAGACAGTGAAGCAAGGAGCAACCTGTGAGACTTCTGAGAGAGAGAGAGAGAGAGAG 1228  
DB 1210 TGAATCATGAGCCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1269  
QY 1229 GAACACCGCTCAGCTCTGAGAGTTTCTGACAGTGGGCGAGAGAGAGAGAGAGAGAG 1288  
DB 1270 GGGGAGAGAGAGTGTCTCTCAAGTTCTGCTAGATGTCTGAGAGAGAGAGAGAGAGAG 1329  
QY 1289 GAGCAAGAGCTGTGTGACAGCGAGCTGAGCGGCGGCAACATCTGTGTCTGAGAGAGCT 1348  
DB 1330 GGGCAACAAATTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1389  
QY 1349 GGTGGCCAAAGTCAAG 1408  
DB 1390 CGTGGCCAAAGTCAAG 1449  
QY 1409 CCGGCTGCGGCTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1468  
DB 1450 CAACCTGCACTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1509  
QY 1469 GTGAGATGTGTGAGATTTTGGGAGTGTCTGTGGAGAGTCTTCATATATGAGAGGCTCC 1528  
DB 1510 GTCTGAGAGTGTGAGATTTTGGAGATCTTCTGTGGAGATATCTCTTTGGGCGAGTGCC 1569  
QY 1529 GTACCTTAAATGTCACTGAAAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1588  
DB 1570 TTATCAAGAAATTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1629  
QY 1589 ACCCGGAGAGGCTGTCCAGAGCGGCTGACAGTCTCATATGAGAGAGAGAGAGAGAG 1648  
DB 1630 TGCCCCGAG 1689  
QY 1649 GCCCGCGCGGCGGAG 1692  
DB 1690 CGCGGAG 1733

RESULT 9  
US-10-187-900-3  
; Sequence 3, Application US/10187/900  
; Publication No. US20030166221A1  
; GENERAL INFORMATION:  
; APPLICANT: BEASLEY, Ellen M. et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; FILE REFERENCE: CLO01061  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; CURRENT APPLICATION NUMBER: US/10/187,900  
; FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 16389  
; TYPE: DNA  
; ORGANISM: Human  
US-10-187-900-3

Query Match 22.8%: Score 455; DB 12; Length 16389;

Best Local Similarity 100.0%; Pred. No. 3.3e-101;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1541 GTCACTGAAAGAGTGTGAGAGCCCTGGAGAAAGGGGTACCCGATGAAACCCCGAGGG 1600  
 Db 13941 GTCACTGAAAGAGTGTGAGAGCCCTGGAGAAAGGGGTACCCGATGAAACCCCGAGGG 14000  
 QY 1601 CTGTCCAGGCCCCGTGTGACAGTCTCATGACAGCTCTGGAGAGAGCCCGCCGCG 1660  
 Db 14001 CTGTCCAGGCCCCGTGTGACAGTCTCATGACAGCTCTGGAGAGAGCCCGCCGCG 14060  
 QY 1661 GGCACCCCTTCCGAAACTGGCCGAGAGTGGCCCGGAGCTACCGAGTGCAGGTGCTCCG 1720  
 Db 14061 GGCACCCCTTCCGAAACTGGCCGAGAGTGGCCCGGAGCTACCGAGTGCAGGTGCTCCG 14120  
 QY 1721 AGCTTCCTGTCTGAGGAGGAGCCGACGCTCTGACCTGCCCCGAAAGCAGAGAGCCCTG 1780  
 Db 14121 AGCTTCCTGTCTGAGGAGGAGCCGACGCTCTGACCTGCCCCGAAAGCAGAGAGCCCTG 14180  
 QY 1781 ACCCCACCCGCTGGGGCCCTTGGCCCGCAGAGACGAGAGTGGAGTGGCGGCTGGG 1840  
 Db 14181 ACCCCACCCGCTGGGGCCCTTGGCCCGCAGAGACGAGAGTGGAGTGGCGGCTGGG 14240  
 QY 1841 GGCACGAGACGAGCCCAAGAGAGGTGACGAGGCGGCAAGTATCTCTGTGGCCACAGC 1900  
 Db 14241 GGCACGAGACGAGCCCAAGAGAGGTGACGAGGCGGCAAGTATCTCTGTGGCCACAGC 14300  
 QY 1901 AGGGGCTGGCCCGACGATGAGGGGCTCTGGGCGCCCTGGACACCCGACAGCTGCAAGA 1960  
 Db 14301 AGGGGCTGGCCCGACGATGAGGGGCTCTGGGCGCCCTGGACACCCGACAGCTGCAAGA 14360  
 QY 1961 TGATGCCCCGATTAAGACGATTTCTAAGACTCTA 1995  
 Db 14361 TGATGCCCCGATTAAGACGATTTCTAAGACTCTA 14395

RESULT 10

US-09-954-456-1983  
 ; Sequence 1983, Application US/0954456  
 ; Patent No. US20020115057A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Paul  
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can  
 ; FILE OF INVENTION: Sets  
 ; FILE REFERENCE: 689290-76  
 ; CURRENT APPLICATION NUMBER: US/09/954,456  
 ; CURRENT FILING DATE: 2001-09-18  
 ; PRIOR APPLICATION NUMBER: US/60/233,617  
 ; PRIOR FILING DATE: 2000-09-18  
 ; PRIOR APPLICATION NUMBER: US/60/234,052  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US/60/234,923  
 ; PRIOR FILING DATE: 2000-09-25  
 ; PRIOR APPLICATION NUMBER: US/60/235,134  
 ; PRIOR FILING DATE: 2000-09-25  
 ; PRIOR APPLICATION NUMBER: US/60/235,637  
 ; PRIOR FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: US/60/235,638  
 ; PRIOR FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: US/60/235,711  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/235,720  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/235,840  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/235,863  
 ; PRIOR FILING DATE: 2000-09-27  
 ; NUMBER OF SEQ ID NOS: 2276  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1983  
 ; LENGTH: 2015  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

US-09-954-456-1983

Query Match 9.6%; Score 192.6; DB 10; Length 2015;  
 Best Local Similarity 54.8%; Pred. No. 2.1e-37;  
 Matches 481; Conservative 0; Mismatches 369; Indels 27; Gaps 4;

QY 812 CTTCGCAACCTCATGATGATGAGATGATTAACAGCAAGAGAGAGGCGCTATCTGCAC 871  
 Db 750 CTTCGCAACCTCATGATGATGAGATGATTAACAGCAAGAGAGAGGCGCTATCTGCAC 809  
 QY 872 CAAGCTGGTGAAGCAAG 931  
 Db 810 GAACTGTGTGCTGCTCCGATGCTTCCAAAGCCCGCAAGAGCTTGGAGAAAGAGTCTTG 869  
 QY 932 GGGGCGCTGTACTGAACCTGACGATTTGACATTTGGAGAGACAGATGAGAGAGAGA 991  
 Db 870 GGAATGCTCTCGGGAATCTCTCAAGC-----TGAGAAAGAACTTGGAGCTGGGA 920  
 QY 992 GTTTGAGCTGTCTGACAGGAGTGAAGTCTGGGCA---AAAGTGGCGTGAAGATAT 1048  
 Db 921 GTTTGGGGAAGTCTGATGAGCACTTCAAAAGCAACCAAGTGGAGTGGAGTGAAGTCA 980  
 QY 1049 CAAG---TGATGATGACAGAGCCAGGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAT 1105  
 Db 981 GAGCCAGGAGAGATGCTGAGAGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGATGAAA 1040  
 QY 1106 GCAACAGAGAACTGTGCTGCTGAGGCGTGAATCTGACACAGAGGCGTGAATGT 1165  
 Db 1041 GAGCATGACAAAGCTGTCAAACTTCACTCGGGTGTACCAAGAGAGAGAGAGAGAGAT 1100  
 QY 1166 CATGAGACGCTGAG 1225  
 Db 1101 CAGGAGTTCATGAG 1160  
 QY 1226 CGTGAACACCGCTGACCTGCTGAGTGTCTGACAGAGAGAGAGAGAGAGAGAGAT 1285  
 Db 1161 GAGCCATGCTGCAAAACTATGATGCTTCTGAGAGAGAGAGAGAGAGAGAGAGATGAT 1220  
 QY 1286 GAG 1345  
 Db 1221 CGAG 1280  
 QY 1346 CCGTGGGCGCAAGTCAAG 1393  
 Db 1281 CCGTGGTGTGAAGTGTGATGCTTGGCTGCGCGGCTGATGAGAGAGAGAGAGAGAG 1340  
 QY 1394 GGGGCTAGACCTCAAGCCGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1453  
 Db 1341 GGGTGGGAG 1400  
 QY 1454 GAAGTTCACGACAG 1513  
 Db 1401 CTCTTCACATCAAG 1460  
 QY 1514 ATATGAG 1573  
 Db 1461 CTACGAG 1520  
 QY 1574 GGGGATACGATGAG 1633  
 Db 1521 TGATACGAG 1580  
 QY 1634 CTGTGGAG 1670  
 Db 1581 CTGTGGAG 1617

RESULT 11

US-10-007-010-3  
 ; Sequence 3, Application US/10007010  
 ; Publication No. US20030125275A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexander H. Borchers







